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WITNESS my hand this
Eleventh day of June 2004

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PROVISIONAL SPECIFICATION

Invention Title: Manipulation of organic acid biosynthesis and secretion 2

The invention is described in the following statement:

MANIPULATION OF ORGANIC ACID BIOSYNTHESIS AND SECRETION 2

The present invention relates to nucleic acid fragments encoding amino acid sequences for organic acid biosynthetic enzymes in plants, and the use thereof for the modification of organic acid biosynthesis and secretion in plants.

5 Documents cited in this specification are for reference purposes only and their inclusion is not acknowledgment that they form part of the common general knowledge in the relevant art.

Organic acids, such as citrate and malate, are key metabolites in plants. They are involved in numerous processes, including C4 and Crassulacean acid
10 metabolism (CAM) photosynthesis, stomatal and pulvinular movement, nutrient uptake, respiration, nitrogen assimilation, fatty acid oxidation, and providing energy to bacteroids in root nodules. For example, malate plays a key role in root nodule metabolism and nitrogen fixation, serving as the primary carbon source for
15 bacteroid maintenance and nitrogenase activity, and is also tightly linked to nodule nitrogen assimilation. Furthermore, the complexing role of organic acids produced and excreted from plant roots has also been associated with tolerance to the aluminium cation Al^{3+} which is toxic to many plants at micromolar concentrations. Aluminium toxicity has been recognized as a major limiting factor of plant
20 productivity on acidic soils, which account for approximately 40% of the earth's arable land.

The tricarboxylic acid cycle (TCA), also known as Krebs cycle (after its discoverer Hans Krebs) or citric acid cycle, moves electrons from organic acids to the oxidized redox cofactors NAD^+ and FAD , forming $NADH$, $FADH_2$, and carbon dioxide (CO_2). The reaction sequence of the TCA cycle involves: in a reaction
25 catalyzed by citrate synthase (CS), acetyl-CoA formed by the pyruvate dehydrogenase complex combines with oxaloacetate to produce the C_6 tricarboxylic acid, citrate. In the overall cycle, the citrate is oxidized to produce two molecules of CO_2 in a series of reactions that leads to the formation of one oxaloacetate, three $NADH$, one $FADH_2$, and one ATP . The resulting oxaloacetate
30 reacts with another molecule of acetyl-CoA to continue the cycle. The oxidative decarboxylation of pyruvate yields an additional CO_2 and $NADH$. Thus the TCA

cycle brings about the complete oxidation of pyruvate to three CO_2 plus 10 electrons, which are stored temporarily as 4 NADH and 1 FADH_2 .

Cytosolic reactions generate products that are transported into the mitochondria to feed the TCA cycle. The nature of the end product of the glycolytic reactions in the cytosol of plants is determined by the relative activities of the three enzymes that can utilize phosphoenol-pyruvate (PEP) as substrate. Both pyruvate kinase and PEP-phosphatase form pyruvate; while PEP-carboxylase (PEPC) generates oxaloacetate. Pyruvate is transported directly into the mitochondrion. Oxaloacetate is either transported directly into the mitochondrion or first reduced to malate by cytosolic malate dehydrogenase (MDH).

Before entering the TCA cycle proper, pyruvate is oxidised and decarboxylated by the pyruvate dehydrogenase enzyme complex to form CO_2 , acetyl-CoA, and NADH. The pyruvate dehydrogenase enzyme complex, which requires the bound cofactors thiamine pyrophosphate, lipoic acid, and FAD as well as free coenzyme A (CoASH) and NAD^+ , links the TCA cycle to glycolysis.

It is known that the TCA cycle includes the following enzymes: pyruvate dehydrogenase, citrate synthase, citrate hydrolase, isocitrate dehydrogenase, oxoglutarate dehydrogenase, succinyl-CoA synthetase, succinate dehydrogenase, fumarase, malate dehydrogenase, NAD-malic enzyme and phosphoenolpyruvate carboxylase.

In particular, citrate synthase (CS) catalyzes the condensation of acetyl-CoA and oxaloacetate to form the C6 molecule citrate and free CoASH, as the TCA cycle proper begins.

Malate dehydrogenase (MDH) catalyzes the final step of the TCA cycle, oxidizing malate to oxaloacetate and producing NADH. This reaction catalyzed by MDH is reversible, thus allowing also for the reversible reduction of oxaloacetate to malate. The enzyme MDH is important in several metabolic pathways, and higher plants contain multiple forms that differ in co-enzyme specificity and subcellular localization. Chloroplasts contain an NADP^+ -dependent MDH that

plays a critical role in balancing reducing equivalents between the cytosol and stroma. Plants also contain NAD-dependent MDHs which are found in a) mitochondria as part of the TCA cycle; b) cytosol and peroxisomes involved in malate-aspartate shuttles; and c) glyoxisomes functioning in β -oxidation. In root nodules of nitrogen-fixing legumes, such as white clover (*Trifolium repens*) and alfalfa (*Medicago sativa*), malate serves as the primary carbon source to support the respiratory needs of the bacterial microsymbiont and the fixation of N_2 by nitrogenase, and a nodule-enhanced MDH is thus critical for nodule function.

Phosphoenolpyruvate carboxylase (PEPC) catalyzes the reaction of phosphoenol-pyruvate with HCO_3^- releasing the phosphate and producing the C_4 product, oxaloacetate. Oxaloacetate is commonly reduced to malate by NADH through the action of malate dehydrogenase (MDH). PEPC is a homotetrameric enzyme widely distributed in most plant tissues. In plants, PEPC fulfils various physiological roles such as the photosynthetic CO_2 fixation in C_4 and Crassulacean Acid Metabolism (CAM) plants, and the anaplerotic pathway.

While nucleic acid sequences encoding some organic acid biosynthetic enzymes have been isolated for certain species of plants, there remains a need for materials useful in modifying organic acid biosynthesis; in modifying organic acid secretion; in modifying phosphorous acquisition efficiency in plants; in modifying aluminium and acid soil tolerance in plants; in modifying nitrogen fixation and nodule function, particularly in forage legumes and grasses, including alfalfa, medic, clovers, ryegrasses and fescues, and for methods for their use.

This invention is directed towards overcoming, or at least alleviating, one or more of the difficulties or deficiencies associated with the prior art.

In one aspect, the present invention provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding the organic acid biosynthetic enzymes CS, MDH and PEPC, from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species, or functionally active fragments or variants thereof.

The present invention also provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding amino acid sequences for a class of proteins from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species which are related to CS, MDH and PEPC, or functionally active fragments or variants thereof. Such proteins are referred to herein as CS-like, MDH-like and PEPC-like respectively.

The present invention also relates to individual or simultaneous enhancement or otherwise manipulation of CS, MDH and/or PEPC or like gene activities in plants to enhance or otherwise alter organic acid biosynthesis; to enhance or reduce or otherwise alter organic acid secretion; to enhance or reduce or otherwise alter phosphorous acquisition efficiency in plants; to enhance or reduce or otherwise alter aluminium and acid soil tolerance in plants; and/or to enhance or reduce or otherwise alter nitrogen fixation and nodule function in legumes.

The individual or simultaneous enhancement or otherwise manipulation of CS, MDH and/or PEPC or like gene activities in plants has significant consequences for a range of applications in, for example, plant production, plant performance, plant nutrition and plant tolerance. For example, it has applications in increasing plant tolerance to aluminium-toxic acid soils; in improving plant nutrient acquisition efficiency for example in increasing acquisition of phosphorus from soils; in increasing nodule function in nitrogen-fixing legumes for example leading to enhanced nitrogen fixation; in modifying the accumulation of organic acids such as citrate in fruits; in modifying the secretion of organic acids for example citrate and/or malate from plant roots.

Manipulation of CS, MDH and/or PEPC or like gene activities in plants, including legumes such as clovers (*Trifolium* species), lucerne (*Medicago sativa*) and grass species such as ryegrasses (*Lolium* species) and fescues (*Festuca* species) may be used to facilitate the production of, for example, forage legumes and forage grasses and other crops with enhanced tolerance to aluminium toxic soils; enhanced nutrient acquisition efficiency; forage legumes with enhanced

nitrogen fixation; fruits with enhanced organic acid content leading to enhanced flavour and health benefits.

The clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species may be of any suitable type, including white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*), alfalfa (*Medicago sativa*), Italian or annual ryegrass (*Lolium multiflorum*), perennial ryegrass (*Lolium perenne*), tall fescue (*Festuca arundinacea*), meadow fescue (*Festuca pratensis*) and red fescue (*Festuca rubra*). Preferably the species is a clover or a ryegrass, more preferably white clover (*T. repens*) or perennial ryegrass (*L. perenne*). White clover (*Trifolium repens* L.) and perennial ryegrass (*Lolium perenne* L.) are key pasture legumes and grasses, respectively, in temperate climates throughout the world. Perennial ryegrass is also an important turf grass.

The nucleic acid or nucleic acid fragment may be of any suitable type and includes DNA (such as cDNA or genomic DNA) and RNA (such as mRNA) that is single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases, and combinations thereof.

The term "isolated" means that the material is removed from its original environment (eg. the natural environment if it is naturally occurring). For example, a naturally occurring nucleic acid or polypeptide present in a living plant is not isolated, but the same nucleic acid or polypeptide separated from some or all of the coexisting materials in the natural system, is isolated. Such an isolated nucleic acid could be part of a vector and/or such a nucleic acid could be part of a composition, and still be isolated in that such a vector or composition is not part of its natural environment. An isolated polypeptide could be part of a composition and still be isolated in that such a composition is not part of its natural environment.

The term "purified" means that the nucleic acid or polypeptide is substantially free of other nucleic acids or polypeptides.

By "functionally active" in respect of a nucleotide sequence it is meant that the fragment or variant is capable of modifying organic acid biosynthesis in a plant. A variant in this context can be an analogue, derivative or mutant and includes naturally occurring allelic variants and non-naturally occurring variants. Additions, deletions, substitutions and derivatizations of one or more of the nucleotides are contemplated so long as the modifications do not result in loss of functional activity of the fragment or variant. Preferably the functionally active fragment or variant has at least approximately 80% identity to the functional part of the above mentioned sequence, more preferably at least approximately 90% identity, most preferably at least approximately 95% identity. Such functionally active variants and fragments include, for example, those having nucleic acid changes which result in conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. Preferably the fragment has a size of at least 30 nucleotides, more preferably at least 45 nucleotides, most preferably at least 60 nucleotides.

By "functionally active" in the context of a polypeptide it is meant that the fragment or variant has one or more of the biological properties of the proteins CS, CS-like, MDH, MDH-like, PEPC and PEPC-like. A variant in this context includes additions, deletions, substitutions and derivatizations of one or more of the amino acids are contemplated so long as the modifications do not result in loss of functional activity of the fragment or variant. Preferably the functionally active fragment or variant has at least approximately 60% identity to the functional part of the above mentioned sequence, more preferably at least approximately 80% identity, most preferably at least approximately 90% identity. Such functionally active variants and fragments include, for example, those having conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. Preferably the fragment has a size of at least 10 amino acids, more preferably at least 15 amino acids, most preferably at least 20 amino acids.

The term "construct" as used herein refers to an artificially assembled or isolated nucleic acid molecule which includes the gene or genes of interest. In general a construct may include the gene or genes of interest, a marker gene which in some cases can also be the gene of interest and appropriate regulatory

sequences. It should be appreciated that the inclusion of regulatory sequences in a construct is optional, for example, such sequences may not be required in situations where the regulatory sequences of a host cell are to be used. The term construct includes vectors but should not be seen as being limited thereto.

- 5 The term "vector" as used herein encompasses both cloning and expression vectors. Vectors are often recombinant molecules containing nucleic acid molecules from several sources.

By "operatively linked" in respect of one or more regulatory elements, nucleic acids or nucleic acid fragments and terminators, is meant that said
10 regulatory element(s) is capable of causing expression of said nucleic acid(s) or nucleic acid fragment(s) in a plant cell and said terminator(s) is capable of terminating expression of said nucleic acid(s) or nucleic acid fragment(s) in a plant cell. Preferably, said regulatory element(s) is upstream of said nucleic acid(s) or nucleic acid fragment(s) and said terminator(s) is downstream of said nucleic
15 acid(s) or nucleic acid fragment(s).

In a particularly preferred embodiment, each nucleic acid or nucleic acid fragment has one or more upstream promoters and one or more downstream terminators, although expression of more than one nucleic acid or nucleic acid fragment from an upstream regulatory element(s) or termination of more than one
20 nucleic acid or nucleic acid fragment from a downstream terminator(s) is not precluded.

By "an effective amount" of a nucleic acid or nucleic acid fragment it is meant an amount sufficient to result in an identifiable phenotypic trait in said plant, or a plant, plant seed or other plant part derived therefrom. Such amounts can be
25 readily determined by an appropriately skilled person, taking into account the type of plant, the route of administration and other relevant factors. Such a person will readily be able to determine a suitable amount and method of administration. See, for example, Maniatis et al, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, the entire disclosure of which is
30 incorporated herein by reference.

It will also be understood that the term "comprises" (or its grammatical variants) as used in this specification is equivalent to the term "includes" and should not be taken as excluding the presence of other elements or features.

Such nucleic acids or nucleic acid fragments could be assembled to form a
5 consensus contig. As used herein, the term "consensus contig" refers to a nucleotide sequence that is assembled from two or more constituent nucleotide sequences that share common or overlapping regions of sequence homology. For example, the nucleotide sequence of two or more nucleic acids or nucleic acid
10 fragments can be compared and aligned in order to identify common or overlapping sequences. Where common or overlapping sequences exist between two or more nucleic acids or nucleic acid fragments, the sequences (and thus their corresponding nucleic acids or nucleic acid fragments) can be assembled into a single contiguous nucleotide sequence.

In a preferred embodiment of this aspect of the invention, the substantially
15 purified or isolated nucleic acid or nucleic acid fragment encoding an CS or CS-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 1, 3, 4, 6, 7, 9, 99, 101, 102 and 104 hereto; (b) complements of the sequences shown in Figures 1, 3, 4, 6, 7, 9, 99, 101, 102 and 104 hereto; (c) sequences antisense to the sequences recited in (a) and (b); and
20 (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding a
MDH or MDH-like protein includes a nucleotide sequence selected from the group
25 consisting of (a) sequences shown in Figures 11, 13, 14, 16, 17, 19, 21, 23, 25, 26, 28, 30, 31, 33, 35, 37, 38, 40, 50, 55, 57, 58, 60, 61, 63, 64, 66, 67, 69, 70, 72, 73, 75, 76, 78, 79, 81, 82 and 84 hereto; (b) complements of the sequences shown in Figures 11, 13, 14, 16, 17, 19, 21, 23, 25, 26, 28, 30, 31, 33, 35, 37, 38, 40, 50, 55, 57, 58, 60, 61, 63, 64, 66, 67, 69, 70, 72, 73, 75, 76, 78, 79, 81, 82 and
30 84 hereto; (c) sequences antisense to the sequences recited in (a) and (b); and (d)

functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an
5 PEPC or PEPC-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 42, 44, 46, 47, 49, 51, 53, 86, 88, 89, 91, 92, 94, 95 and 97 hereto; (b) complements of the sequences shown in Figures 42, 44, 46, 47, 49, 51, 53, 86, 88, 89, 91, 92, 94, 95 and 97 hereto; (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally
10 active fragments and variants of the sequences recited in (a), (b) and (c).

Genes encoding other CS or CS-like, MDH or MDH-like and PEPC or PEPC-like proteins, either as cDNAs or genomic DNAs, may be isolated directly by using all or a portion of the nucleic acids or nucleic acid fragments of the present invention as hybridisation probes to screen libraries from the desired plant
15 employing the methodology well known to those skilled in the art. Specific oligonucleotide probes based upon the nucleic acid sequences of the present invention may be designed and synthesized by methods known in the art. Moreover, the entire sequences may be used directly to synthesize DNA probes by methods known to the skilled artisan such as random primer DNA labelling,
20 nick translation, or end-labelling techniques, or RNA probes using available *in vitro* transcription systems. In addition, specific primers may be designed and used to amplify a part or all of the sequences of the present invention. The resulting amplification products may be labelled directly during amplification reactions or labelled after amplification reactions, and used as probes to isolate full-length
25 cDNA or genomic fragments under conditions of appropriate stringency.

In addition, short segments of the nucleic acids or nucleic acid fragments of the present invention may be used in protocols to amplify longer nucleic acids or nucleic acid fragments encoding homologous genes from DNA or RNA. For example, polymerase chain reaction may be performed on a library of cloned
30 nucleic acid fragments wherein the sequence of one primer is derived from the nucleic acid sequences of the present invention, and the sequence of the other

primer takes advantage of the presence of the polyadenylic acid tracts to the 3' end of the mRNA precursor encoding plant genes. Alternatively, the second primer sequence may be based upon sequences derived from the cloning vector. For example, those skilled in the art can follow the RACE protocol (Frohman *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:8998, the entire disclosure of which is incorporated herein by reference) to generate cDNAs by using PCR to amplify copies of the region between a single point in the transcript and the 3' or 5' end. Using commercially available 3' RACE and 5' RACE systems (BRL), specific 3' or 5' cDNA fragments may be isolated (Ohara *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86:5673; Loh *et al.* (1989) *Science* 243:217, the entire disclosures of which are incorporated herein by reference). Products generated by the 3' and 5' RACE procedures may be combined to generate full-length cDNAs.

In a further aspect of the present invention there is provided a substantially purified or isolated polypeptide from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species, selected from the group consisting of CS or CS-like, MDH or MDH-like and PEPC or PEPC-like proteins; and functionally active fragments and variants thereof.

The clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species may be of any suitable type, including white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*), alfalfa (*Medicago sativa*), Italian or annual ryegrass (*Lolium multiflorum*), perennial ryegrass (*Lolium perenne*), tall fescue (*Festuca arundinacea*), meadow fescue (*Festuca pratensis*) and red fescue (*Festuca rubra*). Preferably the species is a clover or a ryegrass, more preferably white clover (*T. repens*) or perennial ryegrass (*L. perenne*).

In a preferred embodiment of this aspect of the invention, the substantially purified or isolated CS or CS-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in Figures 2, 5, 8, 10, 100 and 103 hereto, and functionally active fragments and variants thereof.

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated MDH or MDH-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in Figures 12, 15, 18, 20, 22, 24, 27, 29, 32, 34, 36, 39, 41, 56, 59, 62, 65, 68, 71, 74, 77, 80, 83 and 85 hereto, and functionally active fragments and variants thereof.

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated PEPC or PEPC-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in Figures 43, 45, 48, 50, 52, 54, 87, 90, 93, 96 and 98 hereto, and functionally active fragments and variants thereof.

In a further embodiment of this aspect of the invention, there is provided a polypeptide recombinantly produced from a nucleic acid or nucleic acid fragment according to the present invention. Techniques for recombinantly producing polypeptides are known to those skilled in the art.

Availability of the nucleotide sequences of the present invention and deduced amino acid sequences facilitates immunological screening of cDNA expression libraries. Synthetic peptides representing portions of the instant amino acid sequences may be synthesized. These peptides may be used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for peptides and/or proteins including the amino acid sequences. These antibodies may be then used to screen cDNA expression libraries to isolate full-length cDNA clones of interest.

A genotype is the genetic constitution of an individual or group. Variations in genotype are important in commercial breeding programs, in determining parentage, in diagnostics and fingerprinting, and the like. Genotypes can be readily described in terms of genetic markers. A genetic marker identifies a specific region or locus in the genome. The more genetic markers, the finer defined is the genotype. A genetic marker becomes particularly useful when it is allelic between organisms because it then may serve to unambiguously identify an

individual. Furthermore, a genetic marker becomes particularly useful when it is based on nucleic acid sequence information that can unambiguously establish a genotype of an individual and when the function encoded by such nucleic acid is known and is associated with a specific trait. Such nucleic acids and/or nucleotide
5 sequence information including single nucleotide polymorphisms (SNPs), variations in single nucleotides between allelic forms of such nucleotide sequence, may be used as perfect markers or candidate genes for the given trait.

Applicants have identified a number of SNPs of the nucleic acids or nucleic acid fragments of the present invention. These are indicated (marked with grey on
10 the black background) in the figures that show multiple alignments of nucleotide sequences of nucleic acid fragments contributing to consensus contig sequences. See for example, Figures 3, 6, 13, 16, 25, 30, 37, 46, 57, 60, 63, 66, 69, 72, 75, 78, 81, 88, 91, 94 101 and 104 hereto.

Accordingly, in a further aspect of the present invention, there is provided a
15 substantially purified or isolated nucleic acid or nucleic acid fragment including a single nucleotide polymorphism (SNP) from a nucleic acid or nucleic acid fragment according to the present invention, for example a SNP from a nucleic acid sequence shown in Figures 3, 6, 13, 16, 25, 30, 37, 46, 57, 60, 63, 66, 69, 72, 75, 78, 81, 88, 91, 94, 101 and 104 hereto; or complements or sequences antisense
20 thereto, and functionally active fragments and variants thereof. The invention further provides a substantially purified or isolated nucleic acid or nucleic acid fragment including a single nucleotide polymorphism (SNP) isolated by the method of this invention.

In a still further aspect of the present invention there is provided a method
25 of isolating a nucleic acid or nucleic acid fragment of the present invention including a SNP, said method including sequencing nucleic acid fragments from a nucleic acid library. The method includes the step of identifying the SNP.

The nucleic acid library may be of any suitable type and is preferably a cDNA library.

The nucleic acid or nucleic acid fragment may be isolated from a recombinant plasmid or may be amplified, for example using polymerase chain reaction.

5 The sequencing may be performed by techniques known to those skilled in the art.

In a still further aspect of the present invention, there is provided use of the nucleic acids or nucleic acid fragments of the present invention including SNPs, and/or nucleotide sequence information thereof, as molecular genetic markers.

10 In a still further aspect of the present invention there is provided use of a nucleic acid or nucleic acid fragment of the present invention, and/or nucleotide sequence information thereof, as a molecular genetic marker.

More particularly, nucleic acids or nucleic acid fragments according to the present invention and/or nucleotide sequence information thereof may be used as a molecular genetic marker for quantitative trait loci (QTL) tagging, QTL mapping, DNA fingerprinting and in marker assisted selection, particularly in clovers, alfalfa, ryegrasses and fescues. Even more particularly, nucleic acids or nucleic acid fragments according to the present invention and/or nucleotide sequence information thereof may be used as molecular genetic markers in plant improvement in relation to plant tolerance to abiotic stresses such aluminium toxic acid soils; in relation to nutrient acquisition efficiency including phosphorus; in relation to nitrogen fixation; in relation to nodulation. Even more particularly, sequence information revealing SNPs in allelic variants of the nucleic acids or nucleic acid fragments of the present invention and/or nucleotide sequence information thereof may be used as molecular genetic markers for QTL tagging and mapping and in marker assisted selection, particularly in clovers, alfalfa, ryegrasses and fescues.

In a still further aspect of the present invention there is provided a construct including one or more nucleic acids or nucleic acid fragments according to the present invention.

In a still further aspect of the present invention there is provided a vector including one or more nucleic acids or nucleic acid fragments according to the present invention.

5 In a preferred embodiment of this aspect of the invention, the vector may include one or several of the following: one or more regulatory elements such as promoters, one or more nucleic acids or nucleic acid fragments according to the present invention and one or more terminators; said one or more regulatory elements, one or more nucleic acids or nucleic acid fragments and one or more terminators being operatively linked.

10 In a preferred embodiment of the present invention the vector may contain nucleic acids or nucleic acid fragments encoding both CS or CS-like and MDH or MDH-like polypeptides, operatively linked to a regulatory element or regulatory elements, such that both CS or CS-like and MDH or MDH-like proteins are expressed.

15 In another preferred embodiment of the present invention the vector may contain nucleic acids or nucleic acid fragments encoding both CS or CS-like and PEPC or PEPC-like polypeptides, operatively linked to a regulatory element or regulatory elements, such that both CS or CS-like and PEPC or PEPC-like proteins are expressed.

20 In yet another particularly preferred embodiment of the present invention the vector may contain nucleic acids or nucleic acid fragments encoding both MDH or MDH-like and PEPC or PEPC-like polypeptides, operatively linked to a regulatory element or regulatory elements, such that both MDH or MDH-like and PEPC or PEPC-like proteins are expressed.

25 In another particularly preferred embodiment of the present invention the vector may contain nucleic acids or nucleic acid fragments encoding all three of CS or CS-like, MDH or MDH-like and PEPC or PEPC-like, operatively linked to a regulatory element or regulatory elements, such that all three of CS or CS-like, MDH or MDH-like and PEPC or PEPC-like proteins are expressed.

The vector may be of any suitable type and may be viral or non-viral. The vector may be an expression vector. Such vectors include chromosomal, non-chromosomal and synthetic nucleic acid sequences, eg. derivatives of plant viruses; bacterial plasmids; derivatives of the Ti plasmid from *Agrobacterium tumefaciens*, derivatives of the Ri plasmid from *Agrobacterium rhizogenes*; phage DNA; yeast artificial chromosomes; bacterial artificial chromosomes; binary bacterial artificial chromosomes; vectors derived from combinations of plasmids and phage DNA. However, any other vector may be used as long as it is replicable, integrative or viable in the plant cell.

- 10 The regulatory element and terminator may be of any suitable type and may be endogenous to the target plant cell or may be exogenous, provided that they are functional in the target plant cell.

Preferably the regulatory element is a promoter. A variety of promoters which may be employed in the vectors of the present invention are well known to those skilled in the art. Factors influencing the choice of promoter include the desired tissue specificity of the vector, and whether constitutive or inducible expression is desired and the nature of the plant cell to be transformed (eg. monocotyledon or dicotyledon). Particularly suitable constitutive promoters include the Cauliflower Mosaic Virus 35S (CaMV 35S) promoter, the maize Ubiquitin promoter, and the rice Actin promoter. Particularly suitable tissue specific promoters include root prevalent promoters.

A variety of terminators which may be employed in the vectors of the present invention are also well known to those skilled in the art. The terminator may be from the same gene as the promoter sequence or a different gene. Particularly suitable terminators are polyadenylation signals, such as the CaMV 35S polyA and other terminators from the nopaline synthase (*nos*) and the octopine synthase (*ocs*) genes.

The vector, in addition to the regulatory element(s), the nucleic acid(s) or nucleic acid fragment(s) of the present invention and the terminator(s), may include further elements necessary for expression of the nucleic acid(s) or nucleic

acid fragment(s), in different combinations, for example vector backbone, origin of replication (ori), multiple cloning sites, spacer sequences, enhancers, introns (such as the maize Ubiquitin *Ubi* intron), antibiotic resistance genes and other selectable marker genes [such as the neomycin phosphotransferase (*npt2*) gene, the
 5 hygromycin phosphotransferase (*hph*) gene, the phosphinothricin acetyltransferase (*bar* or *pat*) gene, the phospho-mannose isomerase (*pmi*) gene], and reporter genes (such as beta-glucuronidase (GUS) gene (*gusA*)]. The vector may also contain a ribosome binding site for translation initiation. The vector may also include appropriate sequences for amplifying expression.

10 As an alternative to use of a selectable marker gene to provide a phenotypic trait for selection of transformed host cells, the presence of the vector in transformed cells may be determined by other techniques well known in the art, such as PCR (polymerase chain reaction), Southern blot hybridisation analysis, histochemical GUS assays, northern and Western blot hybridisation analyses.

15 Those skilled in the art will appreciate that the various components of the vector are operatively linked, so as to result in expression of said nucleic acid(s) or nucleic acid fragment(s). Techniques for operatively linking the components of the vector of the present invention are well known to those skilled in the art. Such techniques include the use of linkers, such as synthetic linkers, for example
 20 including one or more restriction enzyme sites.

The constructs and vectors of the present invention may be incorporated into a variety of plants, including monocotyledons (such as grasses from the genera *Lolium*, *Festuca*, *Paspalum*, *Pennisetum*, *Panicum* and other forage and turfgrasses, corn, oat, sugarcane, wheat and barley), dicotyledons (such as
 25 arabidopsis, tobacco, clovers, medics, eucalyptus, potato, sugarbeet, canola, soybean, chickpea) and gymnosperms. In a preferred embodiment, the constructs and vectors may be used to transform monocotyledons, preferably grass species such as ryegrasses (*Lolium* species) and fescues (*Festuca* species), more preferably perennial ryegrass, including forage- and turf-type cultivars. In an
 30 alternate preferred embodiment, the vectors may be used to transform dicotyledons, preferably forage legume species such as clovers (*Trifolium* species)

and medics (*Medicago* species), more preferably white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*) and alfalfa (*Medicago sativa*). Clovers, alfalfa and medics are key pasture legumes in temperate climates throughout the world.

- 5 Techniques for incorporating the constructs and vectors of the present invention into plant cells (for example by transduction, transfection or transformation) are known to those skilled in the art. Such techniques include *Agrobacterium* mediated introduction, electroporation to tissues, cells and protoplasts, protoplast fusion, injection into reproductive organs, injection into
- 10 immature embryos and high velocity projectile introduction to cells, tissues, calli, immature and mature embryos. The choice of technique will depend largely on the type of plant to be transformed.

Cells incorporating the constructs and vectors of the present invention may be selected, as described above, and then cultured in an appropriate medium to

15 regenerate transformed plants, using techniques well known in the art. The culture conditions, such as temperature, pH and the like, will be apparent to the person skilled in the art. The resulting plants may be reproduced, either sexually or asexually, using methods well known in the art, to produce successive generations of transformed plants.

- 20 In a further aspect of the present invention there is provided a plant cell, plant, plant seed or other plant part, including, e.g. transformed with, one or more constructs, vectors, nucleic acids or nucleic acid fragments of the present invention.

The plant cell, plant, plant seed or other plant part may be from any suitable

25 species, including monocotyledons, dicotyledons and gymnosperms. In a preferred embodiment the plant cell, plant, plant seed or other plant part may be from a monocotyledon, preferably a grass species, more preferably a ryegrass (*Lolium* species) or fescue (*Festuca* species), more preferably perennial ryegrass, including both forage- and turf-type cultivars. In an alternate preferred embodiment

30 the plant cell, plant, plant seed or other plant part may be from a dicotyledon,

preferably forage legume species such as clovers (*Trifolium* species) and medics (*Medicago* species), more preferably white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*) and alfalfa (*Medicago sativa*).

- 5 The present invention also provides a plant, plant seed or other plant part, or a plant extract derived from a plant cell of the present invention.

The present invention also provides a plant, plant seed or other plant part, or a plant extract derived from a plant of the present invention.

- 10 In a further aspect of the present invention there is provided a method of modifying organic acid biosynthesis; of modifying organic acid secretion; of modifying phosphorous and other nutrients acquisition efficiency in plants; of modifying aluminium and acid soil tolerance in plants; of modifying nitrogen fixation and nodule function, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment, construct and/or vector
15 according to the present invention.

- Using the methods and products of the present invention, organic acid biosynthesis; organic acid secretion; phosphorous and other plant nutrient acquisition efficiency; aluminium and acid soil tolerance; nitrogen fixation and nodule function, may be increased or otherwise altered, for example by
20 incorporating additional copies of one or more sense nucleic acids or nucleic acid fragments of the present invention. They may be decreased or otherwise altered, for example by incorporating one or more antisense nucleic acids or nucleic acid fragments of the present invention.

- 25 The present invention will now be more fully described with reference to the accompanying Examples and drawings. It should be understood, however, that the description following is illustrative only and should not be taken in any way as a restriction on the generality of the invention described above.

In the Figures

Figure 1 shows the consensus contig nucleotide sequence of LpCSa.

Figure 2 shows the deduced amino acid sequence of LpCSa.

Figure 3 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpCSa.

5 Figure 4 shows the consensus contig nucleotide sequence of LpCSb.

Figure 5 shows the deduced amino acid sequence of LpCSb.

Figure 6 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpCSb.

Figure 7 shows the nucleotide sequence of LpCSc.

10 Figure 8 shows the deduced amino acid sequence of LpCSc.

Figure 9 shows the nucleotide sequence of LpCSd.

Figure 10 shows the deduced amino acid sequence of LpCSd.

Figure 11 shows the consensus contig nucleotide sequence of LpMDHa.

Figure 12 shows the deduced amino acid sequence of LpMDHa.

15 Figure 13 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHa.

Figure 14 shows the consensus contig nucleotide sequence of LpMDHb.

Figure 15 shows the deduced amino acid sequence of LpMDHb.

20 Figure 16 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHb.

Figure 17 shows the nucleotide sequence of LpMDHc.

Figure 18 shows the deduced amino acid sequence of LpMDHc.

Figure 19 shows the nucleotide sequence of LpMDHd.

Figure 20 shows the deduced amino acid sequence of LpMDHd.

25 Figure 21 shows the nucleotide sequence of LpMDHe.

Figure 22 shows the deduced amino acid sequence of LpMDHe.

Figure 23 shows the consensus contig nucleotide sequence of LpMDHf.

Figure 24 shows the deduced amino acid sequence of LpMDHf.

Figure 25 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHf.

Figure 26 shows the nucleotide sequence of LpMDHg.

5 Figure 27 shows the deduced amino acid sequence of LpMDHg.

Figure 28 shows the consensus contig nucleotide sequence of LpMDHh.

Figure 29 shows the deduced amino acid sequence of LpMDHh.

Figure 30 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHh.

10 Figure 31 shows the nucleotide sequence of LpMDHi.

Figure 32 shows the deduced amino acid sequence of LpMDHi.

Figure 33 shows the nucleotide sequence of LpMDHj.

Figure 34 shows the deduced amino acid sequence of LpMDHj.

Figure 35 shows the consensus contig nucleotide sequence of LpMDHk.

15 Figure 36 shows the deduced amino acid sequence of LpMDHk.

Figure 37 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHk.

Figure 38 shows the nucleotide sequence of LpMDHl.

Figure 39 shows the deduced amino acid sequence of LpMDHl.

20 Figure 40 shows the nucleotide sequence of LpMDHm.

Figure 41 shows the deduced amino acid sequence of LpMDHm.

Figure 42 shows the nucleotide sequence of LpPEPCa.

Figure 43 shows the deduced amino acid sequence of LpPEPCa.

Figure 44 shows the consensus contig nucleotide sequence of LpPEPCb.

25 Figure 45 shows the deduced amino acid sequence of LpPEPCb.

Figure 46 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpPEPCb.

Figure 47 shows the nucleotide sequence of LpPEPCc.

Figure 48 shows the deduced amino acid sequence of LpPEPCc.

Figure 49 shows the nucleotide sequence of LpPEPCd.

Figure 50 shows the deduced amino acid sequence of LpPEPCd.

5 Figure 51 shows the nucleotide sequence of LpPEPCe.

Figure 52 shows the deduced amino acid sequence of LpPEPCe.

Figure 53 shows the nucleotide sequence of LpPEPCf.

Figure 54 shows the deduced amino acid sequence of LpPEPCf.

Figure 55 shows the consensus contig nucleotide sequence of TrMDHa.

10 Figure 56 shows the deduced amino acid sequence of TrMDHa.

Figure 57 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHa.

Figure 58 shows the consensus contig nucleotide sequence of TrMDHb.

Figure 59 shows the deduced amino acid sequence of TrMDHb.

15 Figure 60 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHb.

Figure 61 shows the consensus contig nucleotide sequence of TrMDHc.

Figure 62 shows the deduced amino acid sequence of TrMDHc.

20 Figure 63 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHc.

Figure 64 shows the consensus contig nucleotide sequence of TrMDHd.

Figure 65 shows the deduced amino acid sequence of TrMDHd.

Figure 66 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHd.

25 Figure 67 shows the consensus contig nucleotide sequence of TrMDHe.

Figure 68 shows the deduced amino acid sequence of TrMDHe.

Figure 69 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHe.

Figure 70 shows the consensus contig nucleotide sequence of TrMDHf.

Figure 71 shows the deduced amino acid sequence of TrMDHf.

5 Figure 72 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHf.

Figure 73 shows the consensus contig nucleotide sequence of TrMDHg.

Figure 74 shows the deduced amino acid sequence of TrMDHg.

10 Figure 75 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHg.

Figure 76 shows the consensus contig nucleotide sequence of TrMDHh.

Figure 77 shows the deduced amino acid sequence of TrMDHh.

Figure 78 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHh.

15 Figure 79 shows the consensus contig nucleotide sequence of TrMDHi.

Figure 80 shows the deduced amino acid sequence of TrMDHi.

Figure 81 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHi.

Figure 82 shows the nucleotide sequence of TrMDHj.

20 Figure 83 shows the deduced amino acid sequence of TrMDHj.

Figure 84 shows the nucleotide sequence of TrMDHk.

Figure 85 shows the deduced amino acid sequence of TrMDHk.

Figure 86 shows the consensus contig nucleotide sequence of TrPEPCa.

Figure 87 shows the deduced amino acid sequence of TrPEPCa.

25 Figure 88 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPEPCa.

Figure 89 shows the consensus contig nucleotide sequence of TrPEPCb.

Figure 90 shows the deduced amino acid sequence of TrPEPCb.

Figure 91 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPEPCb.

Figure 92 shows the consensus contig nucleotide sequence of TrPEPCc.

Figure 93 shows the deduced amino acid sequence of TrPEPCc.

5 Figure 94 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPEPCc.

Figure 95 shows the nucleotide sequence of TrPEPCd.

Figure 96 shows the deduced amino acid sequence of TrPEPCd.

Figure 97 shows the nucleotide sequence of TrPEPCe.

10 Figure 98 shows the deduced amino acid sequence of TrPEPCe.

Figure 99 shows the consensus contig nucleotide sequence of TrCSa.

Figure 100 shows the deduced amino acid sequence of TrCSa.

Figure 101 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCSa.

15 Figure 102 shows the consensus contig nucleotide sequence of TrCSb.

Figure 103 shows the deduced amino acid sequence of TrCSb.

Figure 104 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCSb.

EXAMPLE 1

20

Preparation of cDNA libraries, isolation and sequencing of cDNAs coding for CS, CS-like, MDH, MDH-like, PEPC and PEPC-like proteins from white clover (*Trifolium repens*) and perennial ryegrass (*Lolium perenne*)

25

cDNA libraries representing mRNAs from various organs and tissues of white clover (*Trifolium repens*) and perennial ryegrass (*Lolium perenne*) were prepared. The characteristics of the white clover and perennial ryegrass libraries, respectively, are described below (Tables 1 and 2).

TABLE 1
cDNA libraries from white clover (*Trifolium repens*)

Library	Organ/Tissue
01wc	Whole seedling, light grown
02wc	Nodulated root 3, 5, 10, 14, 21 & 28 day old seedling
03wc	Nodules pinched off roots of 42 day old rhizobium inoculated wc
04wc	Nodulated wc cut leaf and stem collected after 0, 1, 4, 6 & 14 h after cutting
05wc	Non-nodulated Inflorescences: <50% open, not fully open and fully open
06wc	Dark grown etiolated
07wc	Inflorescence – very early stages, stem elongation, < 15 petals, 15-20 petals
08wc	seed frozen at -80°C , imbibed in dark overnight at 10°C
09wc	Drought stressed plants
10wc	AMV infected leaf
11wc	WCMV infected leaf
12wc	Phosphorus starved plants
13wc	Vegetative stolon tip
14wc	stolon root initials
15wc	Senescing stolon
16wc	Senescing leaf

TABLE 2
cDNA libraries from perennial ryegrass (*Lolium perenne*)

Library	Organ/Tissue
01rg	Roots from 3-4 day old light-grown seedlings
02rg	Leaves from 3-4 day old light-grown seedlings
03rg	Etiolated 3-4 day old dark-grown seedlings
04rg	Whole etiolated seedlings (1-5 day old and 17 days old)
05rg	Senescing leaves from mature plants
06rg	Whole etiolated seedlings (1-5 day old and 17 days old)
07rg	Roots from mature plants grown in hydroponic culture
08rg	Senescent leaf tissue
09rg	Whole tillers and sliced leaves (0, 1, 3, 6, 12 and 24 h after harvesting)
10rg	Embryogenic suspension-cultured cells
11rg	Non-embryogenic suspension-cultured cells
12rg	Whole tillers and sliced leaves (0, 1, 3, 6, 12 and 24 h after harvesting)
13rg	Shoot apices including vegetative apical meristems
14rg	Immature inflorescences including different stages of inflorescence meristem and inflorescence development
15rg	Defatted pollen
16rg	Leaf blades and leaf sheaths (<i>rbcL</i> , <i>rbcS</i> , <i>cab</i> , <i>wir2A</i> subtracted)
17rg	Senescing leaves and tillers
18rg	Drought-stressed tillers (pseudostems from plants subjected to PEG-simulated drought stress)

Library	Organ/Tissue
19rg	Non-embryogenic suspension-cultured cells subjected to osmotic stress (grown in media with half-strength salts) (1, 2, 3, 4, 5, 6, 24 and 48 h after transfer)
20rg	Non-embryogenic suspension-cultured cells subjected to osmotic stress (grown in media with double-strength salts) (1, 2, 3, 4, 5, 6, 24 and 48 h after transfer)
21rg	Drought-stressed tillers (pseudostems from plants subjected to PEG-simulated drought stress)
22rg	Spikelets with open and maturing florets
23rg	Mature roots (specific subtraction with leaf tissue)

The cDNA libraries may be prepared by any of many methods available. For example, total RNA may be isolated using the Trizol method (Gibco-BRL, USA) or the RNeasy Plant Mini kit (Qiagen, Germany), following the manufacturers' instructions. cDNAs may be generated using the SMART PCR cDNA synthesis kit (Clontech, USA), cDNAs may be amplified by long distance polymerase chain reaction using the Advantage 2 PCR Enzyme system (Clontech, USA), cDNAs may be cleaned using the GeneClean spin column (Bio 101, USA), tailed and size fractionated, according to the protocol provided by Clontech. The cDNAs may be introduced into the pGEM-T Easy Vector system 1 (Promega, USA) according to the protocol provided by Promega. The cDNAs in the pGEM-T Easy plasmid vector are transfected into *Escherichia coli* Epicurian coli XL10-Gold ultra competent cells (Stratagene, USA) according to the protocol provided by Stratagene.

Alternatively, the cDNAs may be introduced into plasmid vectors for first preparing the cDNA libraries in Uni-ZAP XR vectors according to the manufacturer's protocol (Stratagene Cloning Systems, La Jolla, CA, USA). The Uni-ZAP XR libraries are converted into plasmid libraries according to the protocol provided by Stratagene. Upon conversion, cDNA inserts will be contained in the

plasmid vector pBluescript. In addition, the cDNAs may be introduced directly into pre-cut pBluescript II SK(+) vectors (Stratagene) using T4 DNA ligase (New England Biolabs), followed by transfection into *E. coli* DH10B cells according to the manufacturer's protocol (GIBCO BRL Products).

- 5 Once the cDNA inserts are in plasmid vectors, plasmid DNAs are prepared from randomly picked bacterial colonies containing recombinant plasmids, or the insert cDNA sequences are amplified via polymerase chain reaction using primers specific for vector sequences flanking the inserted cDNA sequences. Plasmid DNA preparation may be performed robotically using the Qiagen QiaPrep Turbo kit
10 (Qiagen, Germany) according to the protocol provided by Qiagen. Amplified insert DNAs are sequenced in dye-terminator sequencing reactions to generate partial cDNA sequences (expressed sequence tags or "ESTs"). The resulting ESTs are analyzed using an Applied Biosystems ABI 3700 sequence analyser.

EXAMPLE 2

15 DNA sequence analyses

- The cDNA clones encoding CS, CS-like, MDH, MDH-like, PEPC and PEPC-like proteins were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul *et al.* (1993) *J. Mol. Biol.* 215:403-410) searches. The cDNA sequences obtained were analysed for similarity to all publicly available DNA
20 sequences contained in the eBioinformatics nucleotide database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the SWISS-PROT protein sequence database using BLASTx algorithm (v 2.0.1) (Gish and
25 States (1993) *Nature Genetics* 3:266-272) provided by the NCBI.

- The cDNA sequences obtained and identified were then used to identify additional identical and/or overlapping cDNA sequences generated using the BLASTN algorithm. The identical and/or overlapping sequences were subjected to a multiple alignment using the CLUSTALw algorithm, and to generate a consensus
30 contig sequence derived from this multiple sequence alignment. The consensus contig sequence was then used as a query for a search against the SWISS-PROT

protein sequence database using the BLASTx algorithm to confirm the initial identification.

Finally, it is to be understood that various alterations, modifications and/or additions may be made without departing from the spirit of the present invention as
5 outlined herein.

Agriculture Victoria Services Pty Ltd

AgResearch Limited

By their Registered Patent Attorneys

Freehills Carter Smith Beadle

10 March 2004

Figure 1 Consensus contig nucleotide sequence of LpCSa

```

      *      20      *      40      *      60
LpCSa : GNNTTATATTGACGGGGATGAGGGAATTCTTCGCTACAGAGGCTATCCAATTGAGGAGGT : 60

      *      80      *      100     *      120
LpCSa : GGCTGAAAGCAGCTCGTTTGAGGTGCCTACCTCTTAATGTATGGGAATTTGCCAC : 120

      *      140     *      160     *      180
LpCSa : CCAGAGTCAACTGGCAGGCTGGGAGTTGCAATTTCGCAGCACTCTGCTGTTTCCTCAAGG : 180

      *      200     *      220     *      240
LpCSa : ACTCTTGGATATAATAACAATCAATGCCTCATGATGCCACCCCATGGGTGTCCTTGCCAG : 240

      *      260     *      280     *      300
LpCSa : TGCAATGAGCACACTTTCAGTCTTCCATCCAGATGCAAACCCTGCTCTTAGAGGTCAAGA : 300

      *      320     *      340     *      360
LpCSa : TCTATACAAGTCGAAGCAGGTTAGGGATAAGCAAATTGTACGAGTTCTTGGAAGGCACC : 360

      *      380     *      400     *      420
LpCSa : AGTAATAGCAGCTGCAGCCTATCTGAGATTAGCAGGAAGGCCCTTTGTCCTTCCTTCAAA : 420

      *      440     *      460     *      480
LpCSa : TAATCTCTCTTATTCAGAAAATTTCTTGTATATGCTGGACTCTATGGGTGACAAAGATTA : 480

      *      500     *      520     *      540
LpCSa : TAAGCCAAATCCCAGACTTGCCCGGGTTCTGGATGTCCTTTTATTCTTCATGCTGAACA : 540

      *      560     *      580     *      600
LpCSa : CGAAATGAAC TGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTGATGTCTT : 600

      *      620     *      640     *      660
LpCSa : CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA : 660

      *      680     *      700     *      720
LpCSa : GGCGGTACTTAAAATGTTAAATGAGATTGGAAGTGTAGAGAATATTCGGAATTCATTGA : 720

      *      740     *      760     *      780
LpCSa : GGGAGTGAAGAACAGGAAGCGGAAAATGTCTGGTTTTGGGCACCGTGTGTATAAGAATTA : 780

      *      800     *      820     *      840
LpCSa : TGATCCTCGTGCTAAAGTCATCCGGAAGTTAGCGGAGGAGGTTTTACGATTGTGGGACG : 840

      *      860     *      880     *      900
LpCSa : GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT : 900

      *      920     *      940     *      960
LpCSa : TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT : 960

```

* 980 * 1000 * 1020
 LpCSa : GGGATTCCCTACAGAGTTTTTCCCTGTTCTGTTTGCAGTTCCTCGCATGGCTGGTTGGTT : 1020

* 1040 * 1060 * 1080
 LpCSa : AGCACATTGGAAGGAGTCACTTGATGACCCCGACAATAAAATTATGAGGCCCAACAGGT : 1080

* 1100 * 1120 * 1140
 LpCSa : ATACACCGGTACTTGGCTAAGGCATTACACCCAGTGAGAGAACGGGTGCCATCAAGCGA : 1140

* 1160 * 1180 * 1200
 LpCSa : CAGTGAGCAGCTTGGGCAGATCGCTACATCAAACGCGACGAGGCGTCGGCGTGCTGGCTC : 1200

* 1220 * 1240 * 1260
 LpCSa : TGCCCTGTAGAACAGTCTGCATGATACAGCATAAGTCCACACAATAAACCAAGCTGCCA : 1260

* 1280 * 1300 * 1320
 LpCSa : AGGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATATAGGC : 1320

* 1340 * 1360 * 1380
 LpCSa : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 1380

* 1400 * 1420 * 1440
 LpCSa : TGCACTTGTAACGTGTTGTTAATTTGTTATCCTGCAATGTACGCTCTATAAACTGTTTCAG : 1440

* 1460 * 1480 * 1500
 LpCSa : TATCTTGAAAGTCTTAATCATGTGGACCAATGAAGACATAGATCAAGTTCTTTGCATGGG : 1500

* 1520 * 1540 *
 LpCSa : CGGCGGCTGTTTCTTTGGGAAAAAACTTTTTATGGGAGTCTTTTTTTTACC : 1550

Figure 2 Deduced amino acid sequence of LpCSa

LpCSa : YIDGDEGILRYRGYPIDEEVAESSSFVEVAYLLMYGNLPTQSQLAGWEFAISQHSAPVQGL : 60

LpCSa : LDIIQSMPHDAHPMGVLASAMSTLSVFHPDANPALRGQDLYKSKQVRDKQIVRVLGKAPV : 120

LpCSa : IAAAAYLRLAGRPFVLPNNLSYSENFLYMLDSMGDKDYKPNPRLARVLDVLFILHAEHE : 180

LpCSa : MNCSTAAVRHLASSGVDVFTALSGAVGALYGPLHGGANEAVLKMLNEIGSVENIPEFIEG : 240

LpCSa : VKNRKRKMSGFGHRVYKNYDPRAKVIRKLAEVFTIVGRDPLIEVAVALEKAALSDEYFI : 300

LpCSa : KRKLYPNVDFYSGLIYRAMGFPTTEFFPVLFVPRMAGWLAHWKESLDDPDNKIMRPQQVY : 360

LpCSa : TGTWLRHYTPVRERVPSSEQLGQIATSNATRRRRAGSAL : 401

Figure 3 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpCSa

	*	20	*	40	*	60	
LpCSa1 :		GNNTTATATTGACGGGGATGAGGGAATTCTTCGCTACAGAGGCTATCQAATTGAGGAGGT				:	60
LpCSa2 :		-----				:	-
LpCSa3 :		-----				:	-
LpCSa4 :		-----				:	-
LpCSa5 :		-----				:	-
LpCSa6 :		-----				:	-
LpCSa7 :		-----				:	-
LpCSa8 :		-----				:	-

	*	80	*	100	*	120	
LpCSa1 :		GGCTGAAAGCAGCTCGTTTGTGAGGTCGCCTACCTCTTAATGTATGGGAATTGCCCAC				:	120
LpCSa2 :		-----				:	-
LpCSa3 :		-----				:	-
LpCSa4 :		-----				:	-
LpCSa5 :		-----				:	-
LpCSa6 :		-----				:	-
LpCSa7 :		-----				:	-
LpCSa8 :		-----				:	-

	*	140	*	160	*	180	
LpCSa1 :		CCAGAGTCAACTGGCAGGCTGGGAGTTTGCAATTTGCGAGCACTCTGCTGTTCTCAAGG				:	180
LpCSa2 :		-----GCAGGCTGGGAGTTTGCAATTTGCGCA-----CACTCTGCTGTTCTCANGN				:	46
LpCSa3 :		-----				:	-
LpCSa4 :		-----				:	-
LpCSa5 :		-----				:	-
LpCSa6 :		-----				:	-
LpCSa7 :		-----				:	-
LpCSa8 :		-----				:	-

	*	200	*	220	*	240	
LpCSa1 :		ACTCTTGGATATAATAACAATCAATGCCTCATGATGCCCCACCCCATGGGTGTCCTTGCCAG				:	240
LpCSa2 :		ACTCTTGGATATAATAACAATCAATGCCTCATGATGCCCCACCCCATGGGTGTCCTTGCCAG				:	106
LpCSa3 :		-----				:	-
LpCSa4 :		-----				:	-
LpCSa5 :		-----				:	-
LpCSa6 :		-----				:	-
LpCSa7 :		-----				:	-
LpCSa8 :		-----				:	-

	*	260	*	280	*	300	
LpCSa1 :		TGCAATGAGCACACTTTCAGTCTTCCATCCAGATGCAAACCCTGCTCTTAGAGGTCAAGA				:	300
LpCSa2 :		TGCAATGAGCACACTTTCAGTCTTCCATCCAGATGCAAACCCTGCTCTTAGAGGTCAAGA				:	166
LpCSa3 :		-----				:	-
LpCSa4 :		-----				:	-
LpCSa5 :		-----				:	-
LpCSa6 :		-----				:	-
LpCSa7 :		-----				:	-
LpCSa8 :		-----				:	-

	*	320	*	340	*	360	
LpCSa1 :		TCTATACAAGTCGAAGCAGGTTAGGGATAAGCAAATTGTACGAGTTCTTGGGAAGGCACC					: 360
LpCSa2 :		TCTATACAAGTCGAAGCAGGTTAGGGATAAGCAAATTGTACGAGTTCTTGGGAAGGCACC					: 226
LpCSa3 :		-----					: -
LpCSa4 :		-----					: -
LpCSa5 :		-----					: -
LpCSa6 :		-----					: -
LpCSa7 :		-----					: -
LpCSa8 :		-----					: -

	*	380	*	400	*	420	
LpCSa1 :		AGTAATAGCAGCTGCAGCCTATCTGAGATTAGCAGGAAGGCCCTTTTGTTCCTTCCTTCAAA					: 420
LpCSa2 :		AGTAATAGCAGCTGCAGCCTATCTGAGATTAGCAGGAAGGCCCTTTTGTTCCTTCCTTCAAA					: 286
LpCSa3 :		-----					: -
LpCSa4 :		-----					: -
LpCSa5 :		-----					: -
LpCSa6 :		-----					: -
LpCSa7 :		-----					: -
LpCSa8 :		-----					: -

	*	440	*	460	*	480	
LpCSa1 :		TAATCTCTCTTATTCAGAAAATTTCTTGTATATGCTGGACTCTATGGGTGACAAAGATTA					: 480
LpCSa2 :		TAATCTCTCTTATTCAGAAAATTTCTTGTATATGCTGGACTCTATGGGTGACAAAGATTA					: 346
LpCSa3 :		-----					: -
LpCSa4 :		-----					: -
LpCSa5 :		-----					: -
LpCSa6 :		-----					: -
LpCSa7 :		-----					: -
LpCSa8 :		-----					: -

	*	500	*	520	*	540	
LpCSa1 :		TAAGCCAAATCCCAGACTTGCCCGGGTTCTGGATGTCCTTTTTATTCTTCATGCTGAACA					: 540
LpCSa2 :		TAAGCCAAATCCCAGACTTGCCCGGGTTCTGGATGTCCTTTTTATTCTTCATGCTGAACA					: 406
LpCSa3 :		-----				NTTNTGCTG-ACA	: 12
LpCSa4 :		-----					: -
LpCSa5 :		-----					: -
LpCSa6 :		-----					: -
LpCSa7 :		-----					: -
LpCSa8 :		-----					: -

	*	560	*	580	*	600	
LpCSa1 :		CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTGCGATGTCTT					: 600
LpCSa2 :		CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTGCGATGTCTT					: 466
LpCSa3 :		CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTGCGATGTCTT					: 72
LpCSa4 :		-----					: -
LpCSa5 :		-----					: -
LpCSa6 :		-----					: -
LpCSa7 :		-----					: -
LpCSa8 :		-----					: -

	*	620	*	640	*	660	
LpCSa1 :		CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA					: 660
LpCSa2 :		CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA					: 526
LpCSa3 :		CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA					: 132
LpCSa4 :		-----					: -
LpCSa5 :		-----					: -
LpCSa6 :		-----					: -
LpCSa7 :		-----					: -
LpCSa8 :		-----					: -

	*	680	*	700	*	720	
LpCSa1 :		NGCGGTACTT-AAATGTTAAATGAGATTGGAAGTGTAGAGAATATTCCGGAATTCATTGA					: 719
LpCSa2 :		GGCGGTACTTAAAATGTTAAATGAGATTGGAAGTGTAGAGAATATTCCGGAATTCATTGA					: 586
LpCSa3 :		GGCGGTACTTAAAATGTTAAATGAGATTGGAAGTGTAGAGAATATTCCGGAATTCATTGA					: 192
LpCSa4 :		-----					: -
LpCSa5 :		-----					: -
LpCSa6 :		-----					: -
LpCSa7 :		-----					: -
LpCSa8 :		-----					: -

	*	740	*	760	*	780	
LpCSa1 :		GGGAGTGAAGAACAGGAAGCGGAAAATGTCTGGNTTTGGGCACN-----					: 763
LpCSa2 :		GGGAGTGAAGAACAGGAAGCGGAAAATGTCTGGTTTTGGGCACCGTGTGTATAAGAATTA					: 646
LpCSa3 :		GGGAGTGAAGAACAGGAAGCGGAAAATGTCTGGCTTTGGGCACCGTGTGTATAAGAATTA					: 252
LpCSa4 :		-----GA					: 2
LpCSa5 :		-----					: -
LpCSa6 :		-----					: -
LpCSa7 :		-----					: -
LpCSa8 :		-----					: -

	*	800	*	820	*	840	
LpCSa1 :		-----					: -
LpCSa2 :		TGATCCTCGTGCTAAAGTCATCCGGAAGTTAGCGGN-----					: 682
LpCSa3 :		TGATCCTCGTGCTAAAGTCATCCGGAAGTTAGCGGAGGAGGTTTTCAGGATTGTGGGACG					: 312
LpCSa4 :		TTATCCTCGCGCTAAAGTCAT-CCGGAGTTAGCGGAGGAGGTTTTCAGGATTGTGGGACG					: 61
LpCSa5 :		-----GGAAGTTAGCGGAGGAGGTTTTCAGGATTGTGGGACG					: 37
LpCSa6 :		-----					: -
LpCSa7 :		-----					: -
LpCSa8 :		-----					: -

	*	860	*	880	*	900	
LpCSa1 :		-----					: -
LpCSa2 :		-----					: -
LpCSa3 :		GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGTTAGCACTGTGACACGAGTATTT					: 372
LpCSa4 :		GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTGACACGAGTATTT					: 121
LpCSa5 :		GGNTCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTGACACGAGTATTT					: 97
LpCSa6 :		-----TNNCAGACGAGTATTT					: 16
LpCSa7 :		-----GTCAGACGAGTATTT					: 15
LpCSa8 :		-----					: -

	*	920	*	940	*	960	
LpCSa1 :		-----					: -
LpCSa2 :		-----					: -
LpCSa3 :		TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT					: 432
LpCSa4 :		TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT					: 181
LpCSa5 :		TATCGAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT					: 157
LpCSa6 :		TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT					: 76
LpCSa7 :		TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT					: 75
LpCSa8 :		-----					: -

	*	980	*	1000	*	1020	
LpCSa1 :		-----					: -
LpCSa2 :		-----					: -
LpCSa3 :		GGGATTCCCTACAGAGTTTTTCCCTGTTCTGTTTGAGTTTCTCGCATGGCTGGTTGGTT					: 492
LpCSa4 :		GGGATTCCCTACAGAGTTTTTCCCTGTTCTGTTTGAGTTTCTCGCATGGCTGGTTGGTT					: 241
LpCSa5 :		GGGATTCCCTACAGAGTTTTTCCCTGTTCTGTTTGAGTTTCTCGCATGGCTGGTTGGTT					: 217
LpCSa6 :		GGGATTCCCTACAGAGTTTTTCCCTGTTCTGTTTGAGTTTCTCGCATGGCTGGTTGGTT					: 136
LpCSa7 :		GGGATTCCCTACAGAGTTTTTCCCTGTTCTGTTTGAGTTTCTCGCATGGCTGGTTGGTT					: 135
LpCSa8 :		-----					: -

	*	1040	*	1060	*	1080	
LpCSa1 :	-----		-----		-----		-
LpCSa2 :	-----		-----		-----		-
LpCSa3 :		AGCACATTGGAAGGAGTCAC	TTGATGACCCCGACAATAAA	ATTATGAGGCCCAACAGGT			: 552
LpCSa4 :		AGCACATTGGAAGGAGTCAC	TTGATGACCCCGACAATAAA	ATTATGAGGCCCAACAGGT			: 301
LpCSa5 :		AGCACATTGGAAGGAGTCAC	TTGATGACCCCGACAATAAA	ATTATGAGGCCCAACAGGT			: 277
LpCSa6 :		AGCACATTGGAAGGAGTCAC	TTGATGACCCCGACAATAAA	ATTATGAGGCCCAACAGGT			: 196
LpCSa7 :		AGCACATTGGAAGGAGTCAC	TTGATGACCCCGACAATAAA	ATTATGAGGCCCAACAGGT			: 195
LpCSa8 :	-----		-----		-----		-

	*	1100	*	1120	*	1140	
LpCSa1 :	-----		-----		-----		-
LpCSa2 :	-----		-----		-----		-
LpCSa3 :		ATACACCGGTACTTGGCTAAGG	CATTACACCCCACTGAGAGA	ACGGGTGCCATCAAGCGA			: 612
LpCSa4 :		ATACACCGGTACTTGGCTAAGG	CATTACACCCCACTGAGAGA	ACGGGTGCCATCAAGCGA			: 361
LpCSa5 :		ATACACCGGTACTTGGCTAAGG	CATTACACCCCACTGAGAGA	ACGGGTGCCATCAAGCGA			: 337
LpCSa6 :		ATACACCGGTACTTGGCTAAGG	CATTACACCCCACTGAGAGA	ACGGGTGCCATCAAGCGA			: 256
LpCSa7 :		ATACACCGGTACTTGGCTAAGG	CATTACACCCCACTGAGAGA	ACGGGTGCCATCAAGCGA			: 255
LpCSa8 :	-----		-----		-----		-

	*	1160	*	1180	*	1200	
LpCSa1 :	-----		-----		-----		-
LpCSa2 :	-----		-----		-----		-
LpCSa3 :		CAGTGAGCAGCTTGGGCAGATC	ACTACATCAAACGCGACGAGG	CGTTCGGCGTGCTGGGTC			: 672
LpCSa4 :		CAGTGAGCAGCTTGGGCAGATC	CGCTACATCAAACGCGACGAGG	CGTTCGGCGTGCTGGGTC			: 421
LpCSa5 :		CAGTGAGCAGCTTGGGCAGATC	CGCTACATCAAACGCGACGAGG	CGTTCGGCGTGCTGGGTC			: 397
LpCSa6 :		CAGTGAGCAGCTTGGGCAGATC	CGCTACATCAAACGCGACGAGG	CGTTCGGCGTGCTGGGTC			: 316
LpCSa7 :		CAGTGAGCAGCTTGGGCAGATC	CGCTACATCAAACGCGACGAGG	CGTTCGGCGTGCTGGGTC			: 315
LpCSa8 :	-----	GGCAGATCGCT	CATCAAACGCGT	TCGAGGCGTTCGGCGTGCTGGGTC			: 45

	*	1220	*	1240	*	1260	
LpCSa1 :	-----		-----		-----		-
LpCSa2 :	-----		-----		-----		-
LpCSa3 :		TGCCCTGTAGAACAGTCTGCAT	GATACAGCATA	CAGTCCACACAATAAA	ACCAAGCTGCCA		: 732
LpCSa4 :		TGCCCTGTAGAACAGTCTGCAT	GATACAGCATA	CAGTCCACACAATAAA	ACCAAGCTGCCA		: 481
LpCSa5 :		TGCCCTGTAGAACAGTCTGCAT	GATACAGCATA	CAGTCCACACAATAAA	ACCAAGCTGCCA		: 457
LpCSa6 :		TGCCCTGTAGAACAGTCTGCAT	GATACAGCATA	CAGTCCACACAATAAA	ACCAAGCTGCCA		: 376
LpCSa7 :		TGCCCTGTAGAACAGTCTGCAT	GATACAGCATA	CAGTCCACACAATAAA	ACCAAGCTGCCA		: 375
LpCSa8 :		TGCCCTGTAGAACAGTCTGCAT	GATACAGCATA	CAGTCCACACAATAAA	ACCAAGCTGCCA		: 105

	*	1280	*	1300	*	1320	
LpCSa1 :	-----		-----		-----		-
LpCSa2 :	-----		-----		-----		-
LpCSa3 :		AGGGCCACGGCTGCTTAAATN	-----				: 753
LpCSa4 :		AGGGCCACGGCTGCTTAAATCT	GGGAGCTGCTATACTTGTGTT	TATCAGGTATAT	CTAGGC		: 541
LpCSa5 :		AGGGCCACAGCTGCTTAAATCT	GGGAGCTGCTATACTTGTGTT	TATCAGGTATATATAGGC			: 517
LpCSa6 :		AGGGCCACGGCTGCTTAAATCT	GGGAGCTGCTATACTTGTGTT	TATCAGGTATATATAGGC			: 436
LpCSa7 :		AGGGCCACGGCTGCTTAAATCT	GGGAGCTGCTATACTTGTGTT	TATCAGGTATATATAGGC			: 435
LpCSa8 :		AGGGCCACGGCTGCTTAAATCT	GGGAGCTGCTATACTTGTGTT	TATCAGGTATATATAGGC			: 165

	*	1340	*	1360	*	1380	
LpCSa1 :	-----		-----		-----		-
LpCSa2 :	-----		-----		-----		-
LpCSa3 :	-----		-----		-----		-
LpCSa4 :		AATAAACTAATAATGCCGCCAGG	ACACTTCACTGGTGGTCATGT	GAAGTTGGTAGTAGAA			: 601
LpCSa5 :		AATAAACTAATAATGCCGCCAGG	ACACTTCACTGGTGGTCATGT	GAAGTTGGTAGTAGAA			: 577
LpCSa6 :		AATAAACTAATAATGCCGCCAGG	ACACTTCACTGGTGGTCATGT	GAAGTTGGTAGTAGAA			: 496
LpCSa7 :		AATAAACTAATAATGCCGCCAGG	ACACTTCACTGGTGGTCATGT	GAAGTTGGTAGTAGAA			: 495
LpCSa8 :		AATAAACTAATAATGCCGCCAGG	ACACTTCACTGGTGGTCATGT	GAAGTTGGTAGTAGAA			: 225

	*	1400	*	1420	*	1440	
LpCSa1 :	-----		-----		-----		-
LpCSa2 :	-----		-----		-----		-
LpCSa3 :	-----		-----		-----		-
LpCSa4 :	TGCACTTGTAACGTGTTGTTAATTTGTTATCCTGCAATGTACGCTCTATAAACTGTTTCAG						: 661
LpCSa5 :	TGCACTTGTAACGTGTTGTTAATTTGTTATCCTGCAATGTACGCTCTATAAACTGTTTCAG						: 637
LpCSa6 :	TGCACTTGTAACGTGTTGTTAATTTGTTATCCTGCAATGTACGCTCTATAAACTGTTTCAG						: 556
LpCSa7 :	TGCACTTGTAACGTGTTGTTAATTTGTTATCCTGCAATGTACGCTCTATAAACTGTTTCAG						: 555
LpCSa8 :	TGCACTTGTAACGTGTTGTTAATTTGTTATCCTGCAATGTACGCTCTATAAACTGTTTCAG						: 285

	*	1460	*	1480	*	1500	
LpCSa1 :	-----		-----		-----		-
LpCSa2 :	-----		-----		-----		-
LpCSa3 :	-----		-----		-----		-
LpCSa4 :	TGTCTTGAAAGTCTTAATCATGTGGACCAA-GAAGACATAGATCAAGTTCTTTGCATGGG						: 720
LpCSa5 :	TATCTTGAAAGTCTTANTC>NNNNNAAAAA						: 666
LpCSa6 :	TATCTTGAAAGTCTTAATCATGTGGACCAA-GAAGACATAGATCAAGTTCTTTGCATGGG						: 615
LpCSa7 :	TATCTTGAAAGTCTTAATCATGTGGACCAATCAAAAAA						: 597
LpCSa8 :	TATCTTGAAAGTCTTAAAAA						: 310

	*	1520	*	1540	*	
LpCSa1 :	-----		-----		-----	-
LpCSa2 :	-----		-----		-----	-
LpCSa3 :	-----		-----		-----	-
LpCSa4 :	CGGCGGCTGTTTCTTTGNNAAAAA					: 745
LpCSa5 :	-----		-----		-----	-
LpCSa6 :	CGGCGGCTGTTTCTTTGTGTTTCCTCTTTTATGGGAGTCTTTTTTTACC					: 665
LpCSa7 :	-----		-----		-----	-
LpCSa8 :	-----		-----		-----	-

Figure 4 Consensus contig nucleotide sequence of LpCSb

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      *           20           *           40           *           60
LpCSb : CTTCTCCCTGTNACTGCTCTCCAATGACACAGTTTACCACTGGAGTGATGGCACTCCAAG : 60

      *           80           *           100          *           120
LpCSb : TTGAGAGTGAATTTGCAAAGGCTTATGAGAAGGGAATTCATAAATCAAAGTTCTGGGAGC : 120

      *           140          *           160          *           180
LpCSb : CTACATATGAAGATAGCTTAAATTTGATTGCTCGGCTTCCACAAGTGGCTTCATATGTTT : 180

      *           200          *           220          *           240
LpCSb : ACCGGAGAATTTTCAAGGACGGGAAACTATTGCAGCTGATAATACTGGACTACGCAG : 240

      *           260          *           280          *           300
LpCSb : CTAATTTTTCACACATGCTTGGTTTTTGATGACCCCAAATGCTGGAGTTGATGCGCCTAT : 300

      *           320          *           340          *           360
LpCSb : ACATAACAATTCACACTGATCACGAAGGAGGGAATGTTAGTGCTCATGCTGGGCATCTGG : 360

      *           380          *           400          *           420
LpCSb : TTGGAAGTGCTCTGTCAGATCCTTATCTTTCTTTGTCAGCGGCACTGAACGGTTTAGCTG : 420

      *           440          *           460          *           480
LpCSb : GACCACTGCACGGCTTGGCTAATCAGGAAGTGTGTNATGGATCAAATCTGTGATGGAAG : 480

      *           500          *           520          *           540
LpCSb : AAACCGGGAGTAACATTACAACATGATCAGCTTAAAGAATATGTTTGGAAGACACTGAAGA : 540

      *           560          *           580          *           600
LpCSb : GTGGAAAGGTTGTTCTGCTATGGTCATGGAGTTCTACGTAATACAGATCCACGATACT : 600

      *           620          *           640          *           660
LpCSb : CGTGCCAAAGGGAGTTTGCACTGAAGTATTTACCCGAAGACCACTTTTCCAACCTGGTCT : 660

      *           680          *           700          *           720
LpCSb : CCAAGTTGTACGAAGTTGTGCCTCCTATCCTCACCGAGTTAGGCAAGGTAAAAAACCCAT : 720

      *           740          *           760          *           780
LpCSb : GGCCTAATGTTGATGCTCACAGTGGAGTTTTGCTCAACCACTTCGGATTAGTTGAAGCAC : 780

      *           800          *           820          *           840
LpCSb : GGTACTACACTGTCTTGTTCGGCGTCTCAAGGAGCATGGGAATTGGATCTCAGCTCATTT : 840

      *           860          *           880          *           900
LpCSb : GGGACCGTGCCCTCGGCCCTGCCACTTGAAAGACCGAAGAGTGTCAACCATGGAGTGGCTGG : 900

      *           920          *           940          *           960
LpCSb : AAAACCACTGCAAGAAGGCTGCGGCCTGAAGCTACACCAATGCTTCGTTTACAAATCAG : 960

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* 980 * 1000 * 1020
LpCSb : GCCGTCTTTGATGTTAATAATGACTGAGCATAAGTTAGGCATGGTTAGCCTTGTTTTACC : 1020

* 1040 * 1060 * 1080
LpCSb : ATCTTCGTTTTCTGGCCAATAACTGGAGCAAGAGGCTCACAGACGGTAGAATTTGTAA : 1080

* 1100 * 1120 * 1140
LpCSb : CCACCGNTACTTGAACACCGAATCANTTAAATGTCATTTGGCATAAAGAGATTAGGACAT : 1140

* 1160
LpCSb : GACACATAAGTTTTATGTGTCGGCTCGG : 1167

Figure 5 Deduced amino acid sequence of LpCSb .

LpCSb : SPCXCSPMTQFTTGVMALQVESEFAKAYEKGIIHKSKEPTIEDSLNLIARLPQVASVY : 60

LpCSb : RRIFKDGKTIAADNTLDYAANFSHMLGFDDPKMLELMRLYITIHTDHEGGNNSAHAGHLV : 120

LpCSb : GSALSDPYLSFAAALNGLAGPLHGLANQEV LXWIKSVMEETGSNITTDQLKEYVWKTLS : 180

LpCSb : GKVVPGYGHGVLNRNTDPRYSCQREFALKYLPEDPLFQLVSKLYEVVPPILTELGVKNPW : 240

LpCSb : PNVDHSGVLLNHFGLVEARYYTVLFGVSRSMGIGSQLIWDRLGLPLERPKSVTMEWLE : 300

LpCSb : NHCKKAAA : 308

Figure 6 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpCSb

		*	20	*	40	*	60	
LpCSb1 :	CTTCTCCCTGTNACTGCTCTCCAATGACACAGTTTACCACTGGAGTGATGGCACTCCAAG	:	60					
LpCSb2 :	-----	:	-					
LpCSb3 :	-----	:	-					
LpCSb4 :	-----	:	-					
		*	80	*	100	*	120	
LpCSb1 :	TTGAGAGTGAATTTGCAAAGGCTTATGAGAAGGGAATTCATAAATCAAAGTTCTGGGAGC	:	120					
LpCSb2 :	-----	:	-					
LpCSb3 :	-----	:	-					
LpCSb4 :	-----	:	-					
		*	140	*	160	*	180	
LpCSb1 :	CTACATATGAAGATAGCTTAAATTTGATTGCTCGGCTTCCACAAGTGGCTTCATATGTTT	:	180					
LpCSb2 :	-----	:	-					
LpCSb3 :	-----	:	-					
LpCSb4 :	-----	:	-					
		*	200	*	220	*	240	
LpCSb1 :	ACCGGAGAATTTTCAAGGACGGGAAACTATTGCAGCTGATAATACACTGGACTACGCAG	:	240					
LpCSb2 :	-----	:	-					
LpCSb3 :	-----	:	-					
LpCSb4 :	-----	:	-					
		*	260	*	280	*	300	
LpCSb1 :	CTAATTTTTCACACATGCTTGGTTTTGATGACCCCAAATGCTGGAGTTGATGCGCCTAT	:	300					
LpCSb2 :	-----	:	-					
LpCSb3 :	-----	:	-					
LpCSb4 :	-----	:	-					
		*	320	*	340	*	360	
LpCSb1 :	ACATAACAATTCACACTGATCAGGAAGGGAATGTTAGTGCTCATGCTGGGCATCTGG	:	360					
LpCSb2 :	-----	:	-					
LpCSb3 :	-----	:	-					
LpCSb4 :	-----	:	-					
		*	380	*	400	*	420	
LpCSb1 :	TTGGAAGTGCTCTGTCAGATCCTTATCTTTCTTTGCAGCGGCACTGAACGGTTTAGCTG	:	420					
LpCSb2 :	-----	:	-					
LpCSb3 :	-----	:	-					
LpCSb4 :	-----	:	-					
		*	440	*	460	*	480	
LpCSb1 :	GACCACTGCACGGCTTGGCTAATCAGGAAGTGTCTTATGGATCAAATCTGTGATGGAAG	:	480					
LpCSb2 :	-----TATGGAT-NAATCTGTGATGGAAG	:	24					
LpCSb3 :	-----	:	-					
LpCSb4 :	-----	:	-					
		*	500	*	520	*	540	
LpCSb1 :	AAACCGGGAGTAACATTACAACCTGATCAGCTTAAAGAATATGTTTGGAAGACACTGAAGA	:	540					
LpCSb2 :	-AAACCGGGAGTAACATTACAACCTGATCAGCTTAAAGAATATGTTTGGAAGACACTGAAGA	:	83					
LpCSb3 :	-----CTGAAGA	:	7					
LpCSb4 :	-----	:	-					

* 560 * 580 * 600
 LpCSb1 : GTGGAAAGGTTGTTCTGCTATGGTCATGGAGTTCTACGTAATACAGATCCACGATACT : 600
 LpCSb2 : GTGGAAAGGTTGTTCTGCTATGGTCATGGAGTTCTACGTAATACAGATCCACGATACT : 143
 LpCSb3 : GTGGAAAGGTTGTTCTGCTATGGTCATGGAGTTCTACGTAATACAGATCCACGATACT : 67
 LpCSb4 : ----- : -

* 620 * 640 * 660
 LpCSb1 : CGTGCCAAAGGGAGTTTGCCTGAAGTATTTACCTGAAGACCCACTTTTCCAAGTGGTCT : 660
 LpCSb2 : CGTGCCAAAGGGAGTTTGCCTGAAGTATTTACCCGAAGACCCACTTTTCCAAGTGGTCT : 203
 LpCSb3 : CGTGCCAAAGGGAGTTTGCCTGAAGTATTTACCCGAAGACCCACTTTTCCAAGTGGTCT : 127
 LpCSb4 : ----- : -

* 680 * 700 * 720
 LpCSb1 : CCAAGTTGTATGAAGTTGTGCCTCCTATCCTCAGTGAAGTACCAAGGTAAAAAACCCAT : 720
 LpCSb2 : CCAAGTTGTACGAAGTTGTGCCTCCTATCCTCAGGAGTGAAGTACCAAGGTAAAAAACCCAT : 263
 LpCSb3 : CCAAGTTGTACGAAGTTGTGCCTCCTATCCTCAGGAGTGAAGTACCAAGGTAAAAAACCCAT : 187
 LpCSb4 : ----- : -

* 740 * 760 * 780
 LpCSb1 : GGCCTAATGTTGATGCTCACAGTGGAGTTTGTCTCAACCACTTCGGATTAGTTGAACAC : 779
 LpCSb2 : GGCCTAATGTTGATGCTCACAGTGGAGTTTGTCTCAACCACTTCGGATTAGTTGAAGCAC : 323
 LpCSb3 : GGCCTAATGTTGATGCTCACAGTGGAGTTTGTCTCAACCACTTCGGATTAGTTGAAGCAC : 247
 LpCSb4 : ----- : -

* 800 * 820 * 840
 LpCSb1 : GGNACTACACTGNTTGTGNTCGGN----- : 802
 LpCSb2 : GGTACTACACTGTCTTGTTCGGCGTCTCAAGGAGCATGGGAATTGGATCTCAGCCCATTT : 383
 LpCSb3 : GGTACTACACTGTCTTGTTCGGCGTCTCAAGGAGCATGGGAATTGGATCTCAGCTCATTT : 307
 LpCSb4 : -----GTTTGTGGATCCAGCTCATTT : 22

* 860 * 880 * 900
 LpCSb1 : ----- : -
 LpCSb2 : GGGACCGTGCCCTCGGCCTGCCACTTGAAAGACCGAAGAGTGTACCATGGAGTGGCTGG : 443
 LpCSb3 : GGGACCGTGCCCTCGGCCTGCCACTTGAAAGACCGAAGAGTGTACCATGGAGTGGCTGG : 367
 LpCSb4 : GGGTCCGTGCCCTCGGCCTGCCACTTGAAAGACCGAAGAGTGTACCATGGAGTGGCTGG : 82

* 920 * 940 * 960
 LpCSb1 : ----- : -
 LpCSb2 : AAAACCACTGCAAGAAGGCTGCGGCCTGAAGCTACACCAATGCTTCGTTTACAAATCAG : 503
 LpCSb3 : AAAACCACTGCAAGAAGGCTGCGGCCTGAAGCTACACCAATGCTTCGTTTACAAATCAN : 427
 LpCSb4 : AAAACCACTGCAAGAAGGCTGCGGCCTGAAGCTACACCAATGCTTCGTTTACAAATCAG : 142

* 980 * 1000 * 1020
 LpCSb1 : ----- : -
 LpCSb2 : GCCGTCTTTGATGTTAATAATGACTGAGCATAAGTTAGGCATGGTTAGCCTTGTTTTACC : 563
 LpCSb3 : GCCGTCTTTGATGTTAATAATGACTGAGCATAAGTTAGGCATGGTTAGCCTTGTTTTACC : 487
 LpCSb4 : GCCGTCTTTGATGTTAATAATGACTGAGCATAAGTTAGGCATGGTTAGCCTTGTTTTACC : 202

* 1040 * 1060 * 1080
 LpCSb1 : ----- : -
 LpCSb2 : ATCTTCGTTTTCTGCGCAATAACTGGAGCAAGAGGCTTACAGACGGTAGAATTTTGTA : 623
 LpCSb3 : ATCTTCGTTTTCTGCGCAATAACTGGAGCAAGAGGCTTACAGACGGTAGAATTTTGTA : 547
 LpCSb4 : ATCTTCGTTTTCTGCGCAATAACTGGAGCAAGAGGCTTACAGACGGTAGAATTTTGTA : 262

	*	1100	*	1120	*	1140	
LpCSb1 :	-----						-
LpCSb2 :	CCACCGNTACTTGAACACCGAATCANTTAAATGTCATTTGGCATAAAGAGATTAGGACAT						: 683
LpCSb3 :	CCACCGGTACTTG-ACACCGAATNANNTAAATG GN ATTTGGCATAAAGAGATTAGGACAT						: 606
LpCSb4 :	CCACCGTTACTTGAACACCGAATCAGTTAAATGTCATTTGGCATAAAGAGATTAGGACAT						: 322

	*	1160	
LpCSb1 :	-----		-
LpCSb2 :	GACACATAAGTTTTATGTG NC GN TC CGG		: 710
LpCSb3 :	GACACATAAGTTTTATGTGTCGCTCGG		: 633
LpCSb4 :	GACACATAAGTTTTATGTGTCGCTCGA		: 349

Figure 7 Nucleotide sequence of LpCSc

LpCSc : TCNCCGTGGCCANAATNCCCCANCATTCAAATACCGCCCGTCAGCCACCAATCCTCCTAC : 60

LpCSc : CTTCTTATTTCCACCCCAACCGCCCAACATGTGTCTCTCCACCGAANAACACCTGCTAC : 120

LpCSc : CAACGGCCATAGCAACGGCACCAACGGCGCCAATGGCTCCAAGGAAGGCTTCACAGGCGT : 180

LpCSc : CACGACCAGACAGAACCCTCACCTACACACAAGAGCCCATATGCACCTGTTGGCGACTT : 240

LpCSc : TTTGTCAAATGTCGGCCGCTTCAAGATTATCGAGAGCACATTAAGAGAGGGCGAGCAATT : 300

LpCSc : CGCCAACGCCTACTTCGACCTTGAGGCTAAAATCAAGATCGCCAGAGCTCTCGACAACCTT : 360

LpCSc : TGGTGTGACTACATTGAAGTTACCAGCCCTGCTGCCTCTGAGCAGTCAAGAAGGGACTG : 420

LpCSc : CGAAGCCCTCTGCAAGCTCGGATTGAAAGCCAAGATCCTTACCCACGTACGATGCCACAT : 480

LpCSc : GGACGATGCCAGAATCGCTGTCGAGACTGGTGTGACGGCCTCGATGTCGTCATTGGAAC : 540

LpCSc : CTCTGCGTACCTCCGCGAGCACAGCCATGGCAAGGACATGACATACATCAAAAACACAGC : 600

LpCSc : GCTGGAGGTGATTGAGTTTGTCAAGAGCAAGGGAN : 635

Figure 8 Deduced amino acid sequence of LpCSc

* 20 * 40 * 60
LpCSc : XRGXNXPFKYRPSATNPPTFLFPPQPPNMCPPTTEXTPATNGHSNGTNGANGSKEGFTGV : 60

* 80 * 100 * 120
LpCSc : TTRQNPHPTHKSPYAPVGDFLSNVGRFKIIESTLREGGEQFANAYFDLEAKIKIARALDNF : 120

* 140 * 160 * 180
LpCSc : GVDYIEVTSPAASEQSRRDCEALCKLGLKAKILTHVRCHMDDARIAVETGVDGLDVVIGT : 180

* 200 *
LpCSc : SAYLREHSHGKDMTYIKNTALEVIEFVKSKG : 211

Figure 9 Nucleotide sequence of LpCSd

```

      *           20           *           40           *           60
LpCSd : GTGNTATGGCNCANCCAGNANTCCTNCGTNCTGGCTNCCANANNAGNAANAAGCTATCGG : 60

      *           80           *           100          *           120
LpCSd : CAACGACCTCAGCGATCAGGCCATCAAGGACTACCTGTGGTCCACCCTCAAGGCTGGCCA : 120

      *           140          *           160          *           180
LpCSd : AGTCGTTCCCGGTTACGGACACGCCGTTCTCCGCAAGACCGACCCCGCTACGTCTCCCA : 180

      *           200          *           220          *           240
LpCSd : GCGCGAGTTCGCCCAGAAGCACCTTCCCGACGACCCAATGTTCAAGCTCGTCAGTCAGGT : 240

      *           260          *           280          *           300
LpCSd : CTACAAGATCGCCCCTGGTGTCTCACCAGACGACGGCAAGACCAAGAACCCCTACCCCAA : 300

      *           320          *           340          *           360
LpCSd : CGTCGACGCCCCTCCGGTGTCTCCTCCAGTACTACGGCCTCACTGAGCAGAACTACTA : 360

      *           380          *           400          *           420
LpCSd : CACCGTTCTCTTCGGTGTATCCCGTGCGCTCGGTGTCCTTCCCCAGCTTATCATTGACCG : 420

      *           440          *           460          *           480
LpCSd : TGCCGTCGGTGCCCCCATTTGAGAGGCCCAAGTCTTTCAGCACTGAGGCTTACGCCAAGTT : 480

      *           500          *           520          *           540
LpCSd : GGTTGGTGCTAAGTTGTAAGCGCGTTACTGCAACGTGCTCTACAGCCAGGAGAATGTGGA : 540

      *           560          *           580          *           600
LpCSd : GGAATTTGTTTAACATTACAGAGATACCTTGTCCTGTGTAGAAATTGCAATGTAAGGATAGG : 600

      *           620          *
LpCSd : GAATGGGAGCGTTACGGCGCTACATCACTACATTTN : 636

```

Figure 10 Deduced amino acid sequence of LpCSd

LpCSd : XYGXXXXPXXWXPXXXXAIGNDLSDQAIKDYLWSTLKAGQVVPGYGHAVLRKTDPRYVSQ : 60

LpCSd : REFAQKHLPDDPMFKLVSQVYKIAPGVLTEHGKTKNPYPNVDAHSGVLLQYYGLTEQNY : 120

LpCSd : TVLFGVSRALGVLPQLIIDRAVGAPIERPKSFSTEAYAKLVGAKL : 165

Figure 11 Consensus contig nucleotide sequence of LpMDHa

```

      *           20           *           40           *           60
LpMDHa : GGT TGG TTG CTG GTAT CACC ATTCT GCC CTG TTCT CAC AGG CAA CTC CTTC GACTA ATGC : 60

      *           80           *           100          *           120
LpMDHa : ATT GTCTAG TGAAG ACATCA AGGCTCT CACCA AGAGG ACACAG GAGGG TGGGAC AGAAGT : 120

      *           140          *           160          *           180
LpMDHa : TGT TGAGG CAAAGG CTGGA AAGGG ATCTG CAACTT GTCCAT GGC GTATG CTGGC GCAGT : 180

      *           200          *           220          *           240
LpMDHa : TTT TGGT GATGC ATGCTT GAAGGG CTGAA CGGAG TTCCT GACATT GTTGA ATGCT CCTA : 240

      *           260          *           280          *           300
LpMDHa : CGT GCAAT CAACT ATCAG AACTGCC ATTCTT GCCTC CAAGGT GAGGCT CGGGA AGAA : 300

      *           320          *           340          *           360
LpMDHa : TGG AGTCG AGGAAG TGCTTGG TTTGGG TGAGCTG TCGGC CTTTG AGAAG GAAGG TTTGGA : 360

      *           380          *           400          *           420
LpMDHa : AAG TCTCA AGGGT GAGCTCA AGTCTT CAATTG ACAAG GGCAT CGCGTTCGCCA ATGCGAG : 420

      *           440          *           460          *           480
LpMDHa : TTA ATTAAT TTTGC AGATTAT AGCAA ACCAGG TCTAG TTAAG GGGTCTG TTTTGG ACTTT : 480

      *           500          *           520          *           540
LpMDHa : TTG TTCAG TGCTTTT TCTGCC CATCAC GTGGG CATGGA AGATTT GAGCTT CACAATA AAA : 540

      *           560          *           580          *           600
LpMDHa : ATCC GCGCG CGTAAT GCCAC AGAAC ATTACT TGTACA AGAGG GAACTAG TTCGTGT CAAG : 600

      *           620          *           640          *           660
LpMDHa : TTT TGAACT GGTAC ATTAA ACGA ACAATT GCTG ATGCA CTTTG AGAAAA AAAAAATT GGGG : 660

      *           680          *
LpMDHa : GTG ANTCC ATTGG CCTCA AGCCAAAA AAAAAAAA : 696

```

Figure 12 Deduced amino acid sequence of LpMDHa

* 20 * 40 * 60
LpMDHa : VGCWYHHSALFSQATPSTNALSSEDIKALTKRTQEGGTEVVEAKAGKGSATLSMAYAGAV : 60

* 80 * 100 * 120
LpMDHa : FGDACLKGLNGVPDIVECSYVQSTITELPFFASKVRLGKNGVEEVLGLGELSAFEKEGLE : 120

* 140
LpMDHa : SLKGELKSSIDKGIAFANAS : 140

Figure 13 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpMDHa

	*	20	*	40	*	60	
LpMDHa1 :		GTTTGGTTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC				:	60
LpMDHa2 :		-GGTGGTTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC				:	59
LpMDHa3 :		-GTTGGTTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC				:	59
LpMDHa4 :		----GGTTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC				:	56
LpMDHa5 :		-----				:	-
LpMDHa6 :		-----				:	-
LpMDHa7 :		-----				:	-

	*	80	*	100	*	120	
LpMDHa1 :		ATTGTCTAGTGAAGACATCAAGGCTCTCACCAGAGGACACAGGAGGTTGGGACAGAAGT				:	120
LpMDHa2 :		ATTGTCTAGTGAAGACATCAAGGCTCTCACCAGAGGACACAGGAGGTTGGGACAGAAGT				:	119
LpMDHa3 :		ATTGTCTAGTGAAGACATCAAGGCTCTCACCAGAGGACACAGGAGGTTGGGACAGAAGT				:	119
LpMDHa4 :		ATTGTCTAGTGAAGACATCAAGGCTCTCACCAGAGGACACAGGAGGTTGGGACAGAAGT				:	116
LpMDHa5 :		-----GAGGTTGGGACAGAAGT				:	17
LpMDHa6 :		-----				:	-
LpMDHa7 :		-----				:	-

	*	140	*	160	*	180	
LpMDHa1 :		TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCATGGCGTATGCTGGCGCAGT				:	180
LpMDHa2 :		TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCATGGCGTATGCTGGCGCAGT				:	179
LpMDHa3 :		TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCATGGCGTATGCTGGCGCAGT				:	179
LpMDHa4 :		TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCATGGCGTATGCTGGCGCAGT				:	176
LpMDHa5 :		TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCATGGCGTATGCTGGCGCAGT				:	77
LpMDHa6 :		-----				:	-
LpMDHa7 :		-----				:	-

	*	200	*	220	*	240	
LpMDHa1 :		TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA				:	240
LpMDHa2 :		TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA				:	239
LpMDHa3 :		TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA				:	239
LpMDHa4 :		TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA				:	236
LpMDHa5 :		TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA				:	137
LpMDHa6 :		-----				:	-
LpMDHa7 :		-----				:	-

	*	260	*	280	*	300	
LpMDHa1 :		CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA				:	300
LpMDHa2 :		CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA				:	299
LpMDHa3 :		CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA				:	299
LpMDHa4 :		CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA				:	296
LpMDHa5 :		CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA				:	197
LpMDHa6 :		-----GTNANGCTCGGNNAGAA				:	17
LpMDHa7 :		-----AA				:	2

	*	320	*	340	*	360	
LpMDHa1 :		TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCCGCCCTTTGAGAAGGAAGGTTTGGGA				:	360
LpMDHa2 :		TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCCGCCCTTTGAGAAGGAAGGTTTGGGA				:	359
LpMDHa3 :		TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCCGCCCTTTGAGAAGGAAGGTTTGGGA				:	359
LpMDHa4 :		TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCCGCCCTTTGAGAAGGAAGGTTTGGGA				:	356
LpMDHa5 :		TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCCGCCCTTTGAGAAGGAAGGTTTGGGA				:	257
LpMDHa6 :		TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCCGCCCTTTGAGAAGGAAGGTTTGGGA				:	77
LpMDHa7 :		TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCCGCCCTTTGAGAAGGAAGGTTTGGGA				:	62

```

*          380          *          400          *          420
LpMDHa1 : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG : 420
LpMDHa2 : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG : 419
LpMDHa3 : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG : 419
LpMDHa4 : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG : 416
LpMDHa5 : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG : 317
LpMDHa6 : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG : 137
LpMDHa7 : AAGTCTCAAGGGTGAGTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG : 122

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*          440          *          460          *          480
LpMDHa1 : TTAATTAATTTTGCAGATTATAGCAAACCAGGTCTAGTTAAGGGGTCTG---TTG---TTT : 475
LpMDHa2 : TTAATTAATTTTGCAGATTATAGCAAACCAGGTCTAGTTAAGGGGTCTG---TTG---TTT : 474
LpMDHa3 : TTAATTAATTTTGCAGATTATAGCAAACCAGGTCTAGTTAAGGGGTCTG---TTG---TTT : 474
LpMDHa4 : TTAATTAATTTTGCAGATTATAGCAAACCAGGTCTAGTTAAGGGGTCTG---TTG---TTT : 471
LpMDHa5 : TTGATTAAATTTGCAGATTATAGCAAACCAGGTCTAGTTGAGGGGTCTGTTTTTGACTTT : 377
LpMDHa6 : TTGATTAAATTTGCAGATTATAGCAAACCAGGTCTAGTTGAGGGGTCTGTTTTTGACTTT : 197
LpMDHa7 : TTGATTAAATTTGCAGATTATAGCAAACCAGGTCTAGTTGAGGGGTCTGTTTTTGACTTT : 182

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```

*          500          *          520          *          540
LpMDHa1 : TTGTTCACTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTGAGCTTCACAATAAAAA : 535
LpMDHa2 : TTGTTCACTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTGAGCTTCACAATAAAAA : 534
LpMDHa3 : TTGTTCACTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTGAGCTTCACAATAAAAA : 534
LpMDHa4 : TTGTTCACTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTGAGCTTCACAATAAAAA : 531
LpMDHa5 : TTGTTCACTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTGAGCTTCACAATAAAAA : 437
LpMDHa6 : TTGTTCACTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTGAGCTTCACAATAAAAA : 257
LpMDHa7 : TTGTTCACTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTGAGCTTCACAATAAAAA : 242

```

```

*          560          *          580          *          600
LpMDHa1 : ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAAGTCTAGTTTCGTGTCAAG : 595
LpMDHa2 : ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAAGTCTAGTTTCGTGTCAAG : 594
LpMDHa3 : ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAAGTCTAGTTTCGTGTCAAG : 594
LpMDHa4 : ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAAGTCTAGTTTCGTGTCAAG : 544
LpMDHa5 : ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAAGTCTAGTTTCGTGTCAAG : 497
LpMDHa6 : ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAAGTCTAGTTTCGTGTCAAG : 317
LpMDHa7 : ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAAGTCTAGTTTCGTGTCAAG : 302

```

```

*          620          *          640          *          660
LpMDHa1 : TTTTGAACCTGGTACATTAAACGAACAATTGCTGATGCACTTTGAGAAAAA----- : 650
LpMDHa2 : TTTTGAACCTGGTACATTAAACGAACAATTGCTGATGCACTTTGAGAAAAA----- : 649
LpMDHa3 : TTTTGAACCTGGTACATTAAACGAACAATTGCTGATGCACTTTGAGAAAAA----- : 649
LpMDHa4 : ----- : -
LpMDHa5 : TTTTGAACCTGGTACATTAAACGAACAATTGCTGATGCACTTTGAGAAAAA----- : 557
LpMDHa6 : TTTTGAACCTGGTACATTAAACGAACAATTGCTGATGCACTTTGAGAAAAA----- : 377
LpMDHa7 : TTTTGAACCTGGTACATTAAACGAACAATTGCTGATGCACTTTGAGAAAAA----- : 345

```

```

*          680          *
LpMDHa1 : ----- : -
LpMDHa2 : ----- : -
LpMDHa3 : ----- : -
LpMDHa4 : ----- : -
LpMDHa5 : GTGANTCCATTGGNCTNAAGCCNAAAAAAAA----- : 589
LpMDHa6 : TTGATTCCATTGCTTCAAGTTAAGCAANAANA----- : 413
LpMDHa7 : ----- : -

```


Figure 14 Consensus contig nucleotide sequence of LpMDHb

```

      *           20           *           40           *           60
LpMDHb : TTTGGTNCTTTTGGCCGAGCGAGAAAGCTGTTTCGGTGTCAACACCCTTGNGTTGTTTCGTGC : 60

      *           80           *           100          *           120
LpMDHb : TAAAACTTTCCTACGCTGGGAAGGCAAACGTGCCAGTCACTGGGGTGAATGTTTCCTGTTGT : 120

      *           140          *           160           *           180
LpMDHb : TGGTGGCCATGCTGGTGTACTATCCTGCCACAGTTCTCACAGGCTACTCCTGCAAGTAA : 180

      *           200          *           220           *           240
LpMDHb : TGCATTGTCCCATGAGGACCTTAAGGCCCTCACCAAGAGGACACAAGATGGTGGGACGGA : 240

      *           260          *           280           *           300
LpMDHb : AGTTGTTGAAGCAAAGGCTGGAAAGGGCTCAGCAACATTGTCAATGGCATATGCTGGTGC : 300

      *           320          *           340           *           360
LpMDHb : AGTATTTGGAGATGCATGCTTGAAGGGGCTCAATGGAGTTCTTGACATTGTAGAGTGCTC : 360

      *           380          *           400           *           420
LpMDHb : CTTTGTGCAATCAACCGTAACAGAGCTGCCATTCTTTGCCTCCAAGGTAAGGCTCGGCAA : 420

      *           440          *           460           *           480
LpMDHb : GAACGGAGTGGAGGAAGTGATTGGGCTGGGCGAGCTGTCTGCCTTCGAGAAGGAGGGTCT : 480

      *           500          *           520           *           540
LpMDHb : GGAGAGCCTCAAGGGCGAGCTGNTGNCCTCCATCGAGAAGGGTATCAAGTTCGCGCAGGA : 540

      *           560          *           580           *           600
LpMDHb : GAGCTAGTCAACCTGCTCAGATTCTAACACTCCGCACATGAACTCGGTGGGATCTGATGA : 600

      *           620          *           640           *           660
LpMDHb : ATTTTGGTACGACTCCTTTCACTGCCCCCTTCTCCTGGGGACATTGAGGCGTCGNGCTC : 660

      *           680          *           700           *           720
LpMDHb : CACAATAAAATGGCGTGNCTTGTTGCCATACTGAACTGAACTTGTAATACCAGAAAGAGT : 720

      *           740          *           760           *           780
LpMDHb : GAAACCCTGTGCCTTATGTACCACAGTACGGTGAACCCGAAAATCATGAAGGTAGCAGAA : 780

      *           800
LpMDHb : GATTCTGTGGAAGCTTTTTTCTTTTAN : 807

```

Figure 15 Deduced amino acid sequence of LpMDHb

LpMDHb : * 20 * 40 * 60
LpMDHb : LXL LPSEKAVRCHHPXVVRKTFYAGKANVPVTGVNVPVVGGHAGVTILPQFSQATPASN : 60

LpMDHb : * 80 * 100 * 120
LpMDHb : ALSHEDLKALTKRTQDGGTEVVEAKAGKGSATLSMAYAGAVFGDACLKGLNGVPDIVECS : 120

LpMDHb : * 140 * 160 * 180
LpMDHb : FVQSTVTELPFFASKVRLGKNGVEEVIGLGEISAFEKEGLESLKGELXXSIEKGIKFAQE : 180

LpMDHb : S : 181

Figure 16 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpMDHb

	* 20 * 40 * 60	
LpMDHb1 :	TTTGGTNCCTTTTGCCGAG-NANTTAACTGTTTCGGTGTCAACCACCCTTGNGTTGTTTCGTGCT	: 60
LpMDHb2 :	-----GCGAGAGAGCTGTTTGGTGTCAACCACCCTTGTTGTTGTTTCGTGCT	: 44
	* 80 * 100 * 120	
LpMDHb1 :	AAAACCTTTCTACGCTGGGAAGGCAAACGTGCCAGTCACTGGGGTGAATGTTTCCTGTTGTTG	: 121
LpMDHb2 :	AAAACCTTTCTACGCTGGGAAGGCAAACGTGCCGCTCACTGGGGTGAATGTTTCCTGTTGTTG	: 105
	* 140 * 160 * 180	
LpMDHb1 :	GTGGCCATGCTGGTGTACTATCCTGCCACCTGTTCTCACAGGCTACTCCTGCAAGTAATGC	: 182
LpMDHb2 :	GTGGCCATGCTGGTGTACTATCCTGCCACAGTTCTCACAGGCTACTCCTGCAAGTAATGC	: 166
	* 200 * 220 * 240	
LpMDHb1 :	ATTGTCCCATGAGGACTTAAGGCCCTCACCAAGAGGACACAAGATGGTGGGACGGAAGTT	: 243
LpMDHb2 :	ATTGTCCCATGAGGACCTTAAGGCCCTCACCAAGAGGACACAAGATGGTGGGACGGAAGTT	: 227
	* 260 * 280 * 300	
LpMDHb1 :	GTTGAAGCAAAGGCTGGAAAGGGCTCAGCAACATTGTCAATGGCATATGCTGGTGCAGTAT	: 304
LpMDHb2 :	GTTGAAGCAAAGGCTGGAAAGGGCTCAGCAACATTGTCTGATGGCATATGCTGGTGCAGTTT	: 288
	* 320 * 340 * 360	
LpMDHb1 :	TTGGAGATGCATGCTTGAAGGGGCTCAATGGAGTTCCTGACATTGTAGAGTGCTCCTTTGT	: 365
LpMDHb2 :	TTGGAGATGCATGCTTGAAGGGGCTCAATGGAGTTCCTGACATTGTAGAGTGCTCCTTTGT	: 349
	* 380 * 400 * 420	
LpMDHb1 :	GCAATCAACCTGTAACAGAGCTGCCATTCTTTGCCTCCAAGGTAAGGCTCGGCAAGAACGGA	: 426
LpMDHb2 :	GCAATCAACCGTAACAGAGCTGCCATTCTTTGCCTCCAAGGTAAGGCTCGGCAAGAACGGA	: 410
	* 440 * 460 * 480	
LpMDHb1 :	GTGGAGGAAGTGATTGGGCTGGGCGAGCTGTCTGCCTTCGAGAAGGAGGGTCTGGAGAGCC	: 487
LpMDHb2 :	GTGGAGGAAGTGATTGGGCTGGGCGAGCTGTCTGCCTTCGAGAAGGAGGGTCTGGAGAGCC	: 471
	* 500 * 520 * 540	
LpMDHb1 :	TCAAGGGCGAGCTGNTGNCCTCCATCGAGAAGGGTATCAAGTTCGCGCAGGAGAGCTAGTC	: 548
LpMDHb2 :	TCAAGGGCGAGCTGTGTCCTCCATCGAGAAGGGTATCAAGTTCGCTCAGGAGAGCTAGTC	: 532
	* 560 * 580 * 600 *	
LpMDHb1 :	AACCTGCTCAGATTCTGACACTCCGTCACATGAACCTCGGTGGGATCTGATGAATTTTGCTA	: 609
LpMDHb2 :	AACCTGCTCAGATTCTAACACTCCGCACATGAACCTCGGTGGGATCTGATGAATTTTGCTT	: 593
	* 620 * 640 * 660 *	
LpMDHb1 :	CGACTCCTTTCTGCCCCCTTTCTCGTGGGGACATTGAGGCGTCTGNGCTTCACATTTAAAT	: 670
LpMDHb2 :	CGACTCCTTTCTACTGCCCCCTTCTCCTGGGGACATTGAGGCGTCTGCTCCACAATAAAT	: 654
	* 680 * 700 * 720 *	
LpMDHb1 :	GGCGTGNTTGTGTC-CATACTGANTGAGCTTNTATTCTN-----	: 708
LpMDHb2 :	GGCGTGCTTGTGTCCTACTGAACCTGAACCTTGTAATACCAGAAAGAGTGAAACCCTGTGC	: 715

740

*

760

*

780

*

LpMDHb1 : ----- : -
LpMDHb2 : CTTATGTACCACAGTACGGTGAACCCGAAAATCATGAAGGTAGCAGAGAGATTCTGTGGAAG : 776

800

LpMDHb1 : ----- : -
LpMDHb2 : CTTTTTCTTTTAN : 790

Figure 17 Nucleotide sequence of LpMDHc

```

      *           20           *           40           *           60
LpMDHc : GNNGGTNTACCGAGCGCNCATACTTTNGTGGGTGAGGTTCTTGGACTNGACCCAAGAGAT : 60

      *           80           *           100          *           120
LpMDHc : GTCAATGTTCTGTNGNTGGCGGGCATGCCGGAGTTACNATATTGCCACTCCTTTCGCAG : 120

      *           140          *           160          *           180
LpMDHc : GTTAATCCTCCCTGCTCATTACCATGAGGAAATTAGTATCTCACCTTCACAGCATACAG : 180

      *           200          *           220          *           240
LpMDHc : AATGGTGGGACAGAAAGTNGTCGAGGCGAAAGCTGGAGCAGGATCGGNNACTNTTCTATG : 240

      *           260          *           280          *           300
LpMDHc : GCGNATGCGGCAGCTAAATTTGCAGATGCTTGCTNGAGAGGATTGCATGGTGATGCTGGG : 300

      *           320          *           340          *           360
LpMDHc : ATAGNGGANTGCTCTTATGTGGATTCTCAGGTGACGGANCTNTCTTTNTTTGCATCCAAA : 360

      *           380          *           400          *
LpMDHc : GTTCGCCTTGTTGTTCTGGCGTCNAGGAGATCTTGCCACTTGGTCCACTCAACGAGTN : 419

```

Figure 18 Deduced amino acid sequence of LpMDHc

LpMDHc : XGXPSXHTXVGEVLGXDPDVNPXXGGHAGVXILPLLSQVNPFCSTMRKLVSHLSIQ : 60

LpMDHc : NGGTEXVEAKAGAGSXTXSMAAAKFADACXRGLHGDAGIXXCSYVDSQVTXXSXFASK : 120

LpMDHc : VRLGCSGVXEILPLGPLNE : 139

Figure 19 Nucleotide sequence of LpMDHd

```

      *      20      *      40      *      60
LpMDHd : GNGNTTCCGCCAACACAACACCACCGCTCCCCCGTCCGCATCTCTCCCTTTTCGCCTCCAT : 60

      *      80      *      100      *      120
LpMDHd : CGATCCAGATCCCACACACCGCCGCAGCCAGCAACGATGAGGCCGTTCGGCGATGAGATCC : 120

      *      140      *      160      *      180
LpMDHd : GCCGCGCAGCTCCTCCGCCGCCGCAGCTACTCGTCCGCGTCCGGCCAGCCGGAGCGGAAG : 180

      *      200      *      220      *      240
LpMDHd : GTGGCCATCTTCGGCGCGGCCGGCGGGATCGGGCAGCCGCTGGCGCTCCTCATGAAGCTG : 240

      *      260      *      280      *      300
LpMDHd : AACCCGCTCGTCTCCTCCCTCTCCCTCTACGACATCGCCGCCACCCCGGCGTCGCCGCC : 300

      *      320      *      340      *      360
LpMDHd : GACGTCTCCACATCAACTCCCCGGCCCTGGTGAAGGGGTTTCATGGGCGACGATCAGCTC : 360

      *      380      *      400      *      420
LpMDHd : GCGGAGGCGTTGGAGGGGGGCCGACCTCGTCATCATCCCGGCCGGCGTTCCGAGGAAGCCC : 420

      *      440      *      460      *      480
LpMDHd : GGCATGACCAGGGACGATCTCTTCAACATCAACGCCGCATCGTTAAGAACCTCTGCACC : 480

      *      500      *      520      *      540
LpMDHd : GCCATCGCCAAGTACTGCCCCAACGCTCTTATCAACATGATCAGCAACCCTGTGAACTCA : 540

      *      560      *      580      *      600
LpMDHd : ACTGTTCCAATTGCTGCTGAAGTTTTCAAGAAGGCTGGAACCTATGATGAGAAGAAGTTG : 600

      *      620      *      640      *      660
LpMDHd : TTTGGTGTGACCACTCTTGATGTTGTTTCGTGCCAGGACTTTCTATGCTGGGAAGGCTAAT : 660

      *      680      *      700      *      720
LpMDHd : GTACCTGTTACTGGTGTGAACGTTCTGTGTTGGTGGTCATGCTGGTATCACCATTCTG : 720

      *      740      *      760      *
LpMDHd : CCACTGTTCTCACAGGCAACTCCTTCGACTAATGCATTGTCTAGTGAAGACATN : 774

```

Figure 20 Deduced amino acid sequence of LpMDHd

LpMDHd : * 20 * 40 * 60
: XXPPTQHHRSPVRISPFRLHRSRSHTPPQPATMRPSAMRSAAQLLRRRSYSSASGQPERK : 60

LpMDHd : * 80 * 100 * 120
: VAILGAAGGIGQPLALLMKLNPLVSSLSLYDIAATPGVAADVSHINSPALVKGFMGDDQL : 120

LpMDHd : * 140 * 160 * 180
: AEALEGADLVIIPAGVPRKPGMTRDDLFNINAGIVKNLCTAIAKYCPNALINMISNPVNS : 180

LpMDHd : * 200 * 220 * 240
: TVPIAAEVFKKAGTYDEKKLFGVTTLDVVRARTFYAGKANVPVTGVNVPVVGGHAGITIL : 240

LpMDHd : *
: PLFSQATPSTNALSSDX : 258

Figure 21 Nucleotide sequence of LpMDHe

```

      *      20      *      40      *      60
LpMDHe : TCCGTACNATTGCTGCTGAAGTATTTAAAAAAGCTGGGACATACAATCCTAAGAGATTGT : 60

      *      80      *      100     *      120
LpMDHe : TGGGGGTGACAACACTTGATGTAGTGAGAGCCAATACTTTTGTGGGTGAGGTTCTTGGAC : 120

      *      140     *      160     *      180
LpMDHe : TTGACCCAGAGATGTCAATGTTTCCTGTTGTTGGCGGGCATGCCGGAGTTACGATATTAC : 180

      *      200     *      220     *      240
LpMDHe : CACTCCTTTTCGAGGTTAGTCCTCCCTGCTCGTTCACCCCTGAGGAAATTAGTTATCTCA : 240

      *      260     *      280     *      300
LpMDHe : CCTCACGCATACAGAATGGTGGGACAGAAGTTGTGGAGGCGAAAGCAGGAGCAGGATCGG : 300

      *      320     *      340     *      360
LpMDHe : CAACTCTTTCTATGGCGTATGCGGCAGCTAAATTTGCAGATGCTTGCTTGAGAGGATTGC : 360

      *      380     *      400     *      420
LpMDHe : ATGGTGATGCTGGGATAGTGGAGTGCTCTTATGTGGATTCTCAGGTGACCGGAACTGCCT : 420

      *      440     *      460     *      480
LpMDHe : TCTTTGCATCCAAAGTTCGCCTAGGTCGTTCTGGCGTCGAGGAGATCTTGCAACTTGGGT : 480

      *      500     *      520     *      540
LpMDHe : CCACTGAACCAGGTTTTTGAAAGANCTGGACTGGAANAAGGCGAAANAANGAGCTATCCCG : 540

      *      560     *      580     *      600
LpMDHe : AGAGCCTTCCAGAAAGGNTGTGTCATTTTCGTNCAACAAAGTGAGTTACATGCCATCATCT : 600

      *      620     *      640     *      660
LpMDHe : TTGTTGGATGTGCTTCCCCAAAGTTCCAACACACCGTCGNAATTGGCATATANATATTGC : 660

      *      680     *      700     *      720
LpMDHe : TGGTTGGGGCCTTTTGCNTTNATGCAAACAGGCTACCTTNTGGGTGGGGGGGGTCCGTT : 720

      *      740     *      760     *      780
LpMDHe : NTGAAAACTCTTAACATTTTTTTTTACGGTTGNAACAAAATNTNTGAAAAGCCTGAGA : 780

      *      800     *
LpMDHe : ANTATATGATAANTGAANAAAGTTTNNAAAAAAAAN : 816

```

Figure 22 Deduced amino acid sequence of LpMDHe

 * 20 * 40 * 60
LpMDHe : RXIAAEVFKKAGTYNPKRLLGVTTLDVVRANTFVGEVLGLDPRDVNVPVVGGHAGVTILP : 60

 * 80 * 100 * 120
LpMDHe : LLSQVSPPCSFTPEEISYLTSTRIONGGTEVVEAKAGAGSATLSMAYAAAKFADACLRLH : 120

 * 140 * 160 * 180
LpMDHe : GDAGIVECSYVDSQVTGTAFASKVRLGRSGVEEILQLGSTPGFERXGLEXXGEXXSYPE : 180

 * 200 * 220 * 240
LpMDHe : SLPERXCHFXQSELHAIIFVGCASPKFQHTVXIGIXILLVWGLLXXCKQATXWVGVRX : 240

 * 260 *
LpMDHe : EKLLTFFFTVXNKXXEKPEXYMIXEXSXXXK : 271

Figure 23 Consensus contig nucleotide sequence of LpMDHf

```

      *      20      *      40      *      60
LpMDHf : GGGATGATTNATNCAACAAAAATGCTGGGCATTGTCCGATCAATCTGTGAGGGCGTTGCC : 60

      *      80      *      100     *      120
LpMDHf : AAGAGCTGTCCTAATGCAATAGTGAATTTGATCAGCAACCCTGTGAACTCAACTGTCCCC : 120

      *      140     *      160     *      180
LpMDHf : ATTGCGGCAGAAGNTTTCAGAGGGCTGGAACCTACTGCCCCAAACGTCTCCTTGAGAGTG : 180

      *      200     *      220     *      240
LpMDHf : ACAACTCTTGATGTAGCGAGGGCTAACACCTTTGTGGCTGAAGTGCTTGAGNTGATCCT : 240

      *      260     *      280     *      300
LpMDHf : AGAGAAGNCAGTGTTCGGNTGTTGGCGGGCATGCAGGGATCACTATATTGCCCTCCTG : 300

      *      320     *      340     *      360
LpMDHf : NCCCAGGTCAGCCCCCGTGCTCATTCACTCCAGATGAAATCAGCTATTTGACTAACCGC : 360

      *      380     *      400     *      420
LpMDHf : ATACAGAATGGCGGTACCGAAGTTGTTGAGGCAAAGGCTGGAGCAGGCTCTGCAACTTTG : 420

      *      440     *      460     *      480
LpMDHf : TCAATGGCTTTTGCTGCTGCAAAATTCGCCGATGCATGCTTGCGTGGAATGCGTGGTGAT : 480

      *      500     *      520     *      540
LpMDHf : GCTGGCATTGTGGAATGTNCATACGTTGCATCTGAGGTGACAGAGCTGCCGTTCTTTGCA : 540

      *      560     *      580     *      600
LpMDHf : ACAAAGTGAGGTTAGGTCGTGGCGGAGCTGAGGAGATCCTCCCTCTTGGGCCACTGAAT : 600

      *      620     *      640     *      660
LpMDHf : GACTTTGAGAGAGCTGGCCTGGAGAAGGCGAANAAGGAGCTCAGCGAGAGCATCCAGAAG : 660

      *      680     *      700     *      720
LpMDHf : GGTGTGGCGTTCATGAACAAGTGAGATCATATGAATGGATGGATACCCCGCAACCTATAC : 720

      *      740     *      760     *      780
LpMDHf : ATAGATGATGCAAAGACTAAAGAAAGAGTGTGATATAGTGCTCCTATATACCTGTAAAT : 780

      *
LpMDHf : CTCTCCTGCCTGTAAGAA : 798

```

Figure 24 Deduced amino acid sequence of LpMDHf

 * 20 * 40 * 60
LpMDHf : MLGIVRSICEGVAKSCPNAIVNLISNPVNSTVPPIAAEXFKRAGTYCPKRLLGVTTLDDVAR : 60

 * 80 * 100 * 120
LpMDHf : ANTfVAEVLGXDPREXSVXPVGGHAGITILPLLXQVSPPCSFTPDEISYLTNRIQNGGTE : 120

 * 140 * 160 * 180
LpMDHf : VVEAKAGAGSATLSMAFAAAKFADACLGRMRGDAGIVECKYVASEVTLPFFATKVRLLGR : 180

 * 200 * 220
LpMDHf : GGAEELPLGPLNDFERAGLEKAXKELSESIQKGVAFMNK : 220

Figure 25 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpMDHf

	* 20 * 40 * 60	
LpMDHf1 :	GNNNTGATTNATNCAACAAAAATGCTGGGCATTGTCCGATCAATCTGTGAGGGCGTTGCC	: 60
LpMDHf2 :	-GGATGATTATCAACAAAAATGCTGGG-ATTGTCCGATCAATCTGTGAGGGCGTTGCC	: 58
	* 80 * 100 * 120	
LpMDHf1 :	AAGAGCTGTCCTAATGCAATAGTGAATTTGATCAGCAACCCTGTGAACTCAACTGTCCCC	: 120
LpMDHf2 :	AAGAGCTGTCCTAATGCAATAGTGAATTTGATCAGCAACCCTGTGAACTCAACTGTCCCC	: 118
	* 140 * 160 * 180	
LpMDHf1 :	ATTGCGGCANAAAGNTTTCAGAGGGCTGGAACCTACTGCCCCAAACGTCTCCTTGGAGTG	: 180
LpMDHf2 :	ATTGCGGCAGAAAGTTTTCAGAGGGCTGGAACCTACTGCCCCAAACGTCTCCTTGGAGTG	: 178
	* 200 * 220 * 240	
LpMDHf1 :	ACAACTCTTGATGTAGCGAGGGCTAACACCTTTGTGGCTGAAGTGCTTGNAGNTGATCCT	: 240
LpMDHf2 :	ACAACTCTTGATGTAGCGAGGGCTAACACCTTTGTGGCTGAAGTGCTTGGAGTTGATCCT	: 238
	* 260 * 280 * 300	
LpMDHf1 :	AGAGAAGNCAGTGTTCGGGNTGTTGGCGGGCATGCNNGGATCACTATATTGCCCTCCTG	: 300
LpMDHf2 :	AGAGAAGTCAGTGTTCGGGTTGTTGGCGGGCATGCAGGGATCACTATATTGCCCTCCTG	: 298
	* 320 * 340 * 360	
LpMDHf1 :	NCCCAGGTCAGCCCCCGTGCTCATTCACTCCAGATGAAATCAGCTATTTGACTAACCGC	: 360
LpMDHf2 :	CCCAGGTCAGCCCCCGTGCTCATTCACTCCAGATGAAATCAGCTATTTGACTAACCGC	: 358
	* 380 * 400 * 420	
LpMDHf1 :	ATACAGAATGGCGGTACCGAAGTTGTTGAGGCAAAGGCTGGAGCAGGCTCTGCAACTTTG	: 420
LpMDHf2 :	ATACAGAATGGCGGTACCGAAGTTGTTGAGGCAAAGGCTGGAGCAGGCTCTGCAACTTTG	: 418
	* 440 * 460 * 480	
LpMDHf1 :	TCAATGGCTTTTGCTGCTGCAAAATTCGCCGATGCATGCTTGCGTGGAAATGCGTGGTGAT	: 480
LpMDHf2 :	TCAATGGCTTTTGCTGCTGCAAAATTCGCCGATGCATGCTTGCGTGGAAATGCGTGGTGAT	: 478
	* 500 * 520 * 540	
LpMDHf1 :	GCTGGCATTGTGGAATGTTCATACGTTGCATCTGAGGTGACAGAGCTGCCGTTCTTTGCA	: 540
LpMDHf2 :	GCTGGNATTGTGGAATGTN-----	: 497
	* 560 * 580 * 600	
LpMDHf1 :	ACAAAAGTGAGGTTAGGTCGTGGCGGAGCTGAGGAGATCCTCCCTCTGGGGCCACTGAAT	: 600
LpMDHf2 :	-----	: -
	* 620 * 640 * 660	
LpMDHf1 :	GACTTTGAGAGAGCTGGCCTGGAGAAGGCCAANAAGGAGCTCAGCGAGAGCATCCAGAAG	: 660
LpMDHf2 :	-----	: -
	* 680 * 700 * 720	
LpMDHf1 :	GGTGTGGCGTTTCATGAACAAGTGAGATCATATGAATGGATGGATACCCGCAACCTATAC	: 720
LpMDHf2 :	-----	: -

*

740

*

760

*

780

LpMDHf1 : ATAGATGATGCAAAGACTAAAGAAAGAGTGTGATATAGTGCTCCTATATACCTGTAAAAAT : 780
LpMDHf2 : ----- : -

*

LpMDHf1 : CTCTCCTGCCTGTAAGAA : 798
LpMDHf2 : ----- : -

Figure 26 Nucleotide sequence of LpMDHg

```

      *           20           *           40           *           60
LpMDHg : CAATTGCACGTTCTTGCTCACTTCAGCATCACCCCTCAGCTTCTCCTACACAACCCCTCC : 60

      *           80           *           100          *           120
LpMDHg : CAACCGTCACTATGGTCAAGGCTGTCGTGCGAGGTGCTGCTGGTGGTATCGGECAGCCCC : 120

      *           140          *           160          *           180
LpMDHg : TCTCTCTTCTACTCAAGACGAGCCCCCTCATCGATGAGCTTGCCCTCTACGATGTTGTCA : 180

      *           200          *           220          *           240
LpMDHg : AACTCCCGGTGTTGCCGCTGATCTTCCACATCTCATCCGCGCTCAAATCGCCGGCT : 240

      *           260          *           280          *           300
LpMDHg : ACCTCCCAAGGATGATGGCGCAAAGGCTGCATTCAAAGATGCCGACATTATCGTCATCC : 300

      *           320          *           340          *           360
LpMDHg : CCGCCGGCATTCCTCGCAAGCCTGGCATGACCCGTGATGACCTCTTCAACATCAACGCCG : 360

      *           380          *           400          *           420
LpMDHg : GAATTGTCAAGGGTCTGATTGAGGTTGCCGCCGAAGTTGCCCCCAAGGCCTTCATTCTGG : 420

      *           440          *           460          *           480
LpMDHg : TCATCTCCAACCCTGTCAACTCTACCGTCCCTATCTCTGCCGAGGTCTCAAGGCCAAGG : 480

      *           500          *           520          *           540
LpMDHg : GCGTCTTCAACCCTCAGCGTCTTTTCGGTGTCAACCACCTCGACATCGTCCGTGCCGAGA : 540

      *           560          *           580          *           600
LpMDHg : CTTTCGTCGCCAGCATCACCGGCGAGAAGCAGCCCCAGAACTTGACCGTCCCCGTCAATTG : 600

      *           620          *           640          *           660
LpMDHg : GCGGCCACTCCGGCGAGACCATCGTCCCGCTTTTCAGCAAGGNTCAGCCCTCTGCTTNCA : 660

LpMDHg : TTCCCGC : 667

```

Figure 27 Deduced amino acid sequence of LpMDHg

LpMDHg : IARSCSLQHHPHASPTQPLPTVMVKAVVAGAAGGIGQPLSLLLKTSPLIDELALYDVVN : 60

LpMDHg : TPGVAADLSHISSRAQIAGYLPKDDGAKAAFKDADIIVIPAGIPRKPGMTRDDLFNINAG : 120

LpMDHg : IVKGLIEVAAEVAPKAFILVISNPVNSTVPISAEVLKAKGVFNPQRLFGVTTLDIVRAET : 180

LpMDHg : FVASITGEKQPQNLTVPVIGGHSGETIVPLFSKXQPSAXIP : 221

Figure 28 Consensus contig nucleotide sequence of LpMDHh

```

      *           20           *           40           *           60
LpMDHh : TNACGGAGCTGCTTAAATCAGCCCCCATTCGCCTCGTCTATAGCGATCCTTCATCCCGT : 60

      *           80           *           100          *           120
LpMDHh : TGTCGTCGCCTCCTCCCGAACCACTCTCCCATCCCCGAACCTCCAGAACCGGCTCCAATG : 120

      *           140          *           160          *           180
LpMDHh : GCGGCGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCT : 180

      *           200          *           220          *           240
LpMDHh : CTTGTTCCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCAT : 240

      *           260          *           280          *           300
LpMDHh : ATGCTGGATATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGAT : 300

      *           320          *           340          *           360
LpMDHh : GCCGCATTTCCACTTCTCAAGGGAGTTGTTGCAACAACCTGATGTTGTTGAGGCTTGCACT : 360

      *           380          *           400          *           420
LpMDHh : GGTGTGAATGTTGCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAG : 420

      *           440          *           460          *           480
LpMDHh : GATGTTATGTCTAAGAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCAT : 480

      *           500          *           520          *           540
LpMDHh : GCAGCCCCGAATTGCAAGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATC : 540

      *           560          *           580          *           600
LpMDHh : TTAAAGGAGTTTGCTCCATCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGAC : 600

      *           620          *           640          *           660
LpMDHh : CATAACAGGGCACTTGGTCAGATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAG : 660

      *           680          *           700          *           720
LpMDHh : AATGTTATCATCTGGGGCAATCACTCTTCAGTCAGTACCCTGATGTGAACCACGCCACC : 720

      *           740          *           760          *           780
LpMDHh : GTGAAGACTTCCAGTGGCGAGAAGCCTGTTTCGCGAACTTGTTAAAGACGATGAATGGCTA : 780

      *           800          *           820          *           840
LpMDHh : AATGCAGGGTTCATTGCCACTGTCCAGCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAG : 840

      *           860          *           880          *           900
LpMDHh : CTCTCCAGTGCTCTCTCTGCTGCCAGCTCTGCTTGTGACCACATCCGTGATTGGGTTCTC : 900

      *           920          *           940          *           960
LpMDHh : GGAACCCCTGAGGGAACATTTGTTTCCATGGGTGTGTATTCTGATGGTTCATACGGTGTG : 960

```

* 980 * 1000 * 1020
LpMDHh : CCTGCTGGGCTTATCTACTCCTTCCCAGTAACTTGCTGCGGTGGTGAATGGACAATTGTT : 1020

* 1040 * 1060 * 1080
LpMDHh : CAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGAAGATGGATGCCACAGCCCAGGAGCTC : 1080

* 1100 * 1120 * 1140
LpMDHh : TCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAGTAACTGCATACCAGGGAGCAGCTG : 1140

* 1160 * 1180 * 1200
LpMDHh : CCGCTCTGATGTTTTGAATAAAAGGAACATTTTGGCTCCATGAAACTCATCTCCACTCAG : 1200

* 1220 * 1240 * 1260
LpMDHh : AACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAGTGTGTATGAATGAGGCTTTT : 1260

* 1280 * 1300 * 1320
LpMDHh : GTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTGGCAGGAAGATTGGAACAA : 1320

* 1340 * 1360 * 1380
LpMDHh : TTTGACGTCTGATTAAAACCAACCTCTTATTATTCCTGTGTGTATGAATGAGGCTTTTGT : 1380

* 1400 * 1420 * 1440
LpMDHh : AGCTCTATTTTCGCCTGATGATTTACAGGCCATGATATTGGCAGGAGGATTGGAACAATT : 1440

* 1460 * 1480
LpMDHh : TGACGCCTGATTAAAACCAACCTCTTATTACTAAAAAAAAAAAA : 1484

Figure 29 Deduced amino acid sequence of LpMDHh

```

      *      20      *      40      *      60
LpMDHh : MAAKEPMRVLVTGAAGQIGYALVPMIARGIMLGADQPVILHMLDIPPAEALNGVKMELV : 60

      *      80      *      100     *      120
LpMDHh : DAAFPLLKGVVATTDVVEACTGVNVAVMVGGFPRKEGMERKDVMSKNVSIYKSQASALEA : 120

      *      140     *      160     *      180
LpMDHh : HAAPNCKVLVVANPANTNALILKEFAPSIPEKNISCLTRLDHNRALGQISERLDVQVSDV : 180

      *      200     *      220     *      240
LpMDHh : KNVVIWGNHSSSQYPDVNHATVKTSSGEKPVRELVKDDEWLNAGFIATVQQRGAIIKAR : 240

      *      260     *      280     *      300
LpMDHh : KLSSALSAASSACDHIRDWVLGTPEGTFVSMGVYSDGSYGVPAGLIYSFPVTCCGGEWTI : 300

      *      320     *
LpMDHh : VQGLPIDEF SRKKMDATAQELSEEKALAYSCLE : 333

```

Figure 30 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpMDHh

	*	20	*	40	*	60	
LpMDHh1	:	TNACGGAGCTGCTTAAATCAGCCCCCATTCGCGCTCGTCT	-G	-ACTATCCTTCATCCCGTTG	:	60	
LpMDHh2	:	-----	CGGNTTTACCTGT	NONAN	-CG	-CGTSCGTT	: 29
LpMDHh3	:	-----	GNGTAT	CCENTGNTACA	-CENAGCTN	:	24
LpMDHh4	:	-----	GTTTACCGT	INCTAC	-CENAGCTN	:	22
LpMDHh5	:	-----	GNNTACCTTC	GNCCCGTTG	:	20	
LpMDHh6	:	-----	GNNTNCCTTC	GTCCCGTTG	:	19	
LpMDHh7	:	-----	GCTTTT	-CGTTCATCCCGTTG	:	18	
LpMDHh8	:	-----	GCTATCCTTC	CATCCCGTTG	:	19	
LpMDHh9	:	-----	GCTATCCTTC	CATCCCGTTG	:	19	
LpMDHh10	:	-----	NTTACCTTC	GNCCCGTTG	:	18	
LpMDHh11	:	-----	GNNTACCTTC	GTCCCGTTG	:	18	
LpMDHh12	:	-----	CTATCCTTC	ATCCCGTTG	:	17	
LpMDHh13	:	-----	GATCCTTC	ATCCCGTTG	:	16	
LpMDHh14	:	-----	GNNTACCTTC	GTCCCGTTG	:	17	
LpMDHh15	:	-----	GATCCTTC	CATCCCGTTG	:	17	
LpMDHh16	:	-----	GNTCCTTC	CATCCCGTTG	:	17	
LpMDHh17	:	-----	GATCCTTC	ATCCCGTTG	:	16	
LpMDHh18	:	-----	GNTCCTTC	CATCCCGTTG	:	17	
LpMDHh19	:	-----	GNNCCTTC	CATCCCGTTG	:	17	
LpMDHh20	:	-----	GCTCCTTC	NTCCCGTTG	:	16	
LpMDHh21	:	-----	GNTCCTTC	CATCCCGTTG	:	17	
LpMDHh22	:	-----	GATCCTTC	CATCCCGTTG	:	17	
LpMDHh23	:	-----	GNCTTC	ATCCCGTTG	:	16	
LpMDHh24	:	-----	GNTCCTTC	ATCCCGTTG	:	16	
LpMDHh25	:	-----	CTCCTTC	GTCCCGTTG	:	16	
LpMDHh26	:	-----	TCCTTC	ATCCCGTTG	:	15	
LpMDHh27	:	-----	ACCTTC	ATCCCGTTG	:	15	
LpMDHh28	:	-----	TCCTTC	NTCCCGTTG	:	14	
LpMDHh29	:	-----	TCCTTC	ATCCCGTTG	:	14	
LpMDHh30	:	-----	TCCTTC	NTCCCGTTG	:	15	
LpMDHh31	:	-----	CCCTTC	CATCCCGTTG	:	14	
LpMDHh32	:	-----	NCCTTC	TCCCGTTG	:	14	
LpMDHh34	:	-----	ACCTTC	ATCCCGTTG	:	14	
LpMDHh35	:	-----	CTTC	GTCCCGTTG	:	13	
LpMDHh36	:	-----	TTNC	ATCCCGTTG	:	13	
LpMDHh37	:	-----	TTNC	ATCCCGTTG	:	13	
LpMDHh38	:	-----	NTTC	ATCCCGTTG	:	13	
LpMDHh39	:	-----	TTTC	ATCCCGTTG	:	12	
LpMDHh40	:	-----	TTTC	ATCCCGTTG	:	12	
LpMDHh41	:	-----	NTTC	ATCCCGTTG	:	12	
LpMDHh42	:	-----	NTTC	ATCCCGTTG	:	12	
LpMDHh43	:	-----	GTTC	ATCCCGTTG	:	12	
LpMDHh44	:	-----	TTTC	ATCCCGTTG	:	11	
LpMDHh45	:	-----	TTTC	ATCCCGTTG	:	11	
LpMDHh46	:	-----	TTTC	ATCCCGTTG	:	11	
LpMDHh47	:	-----	TTCCCGTTG	:	8		
LpMDHh48	:	-----	CGTTG	:	5		
LpMDHh49	:	-----	CCGTTG	:	6		
LpMDHh50	:	-----		:	-		
LpMDHh51	:	-----		:	-		
LpMDHh52	:	-----		:	-		
LpMDHh53	:	-----		:	-		
LpMDHh54	:	-----		:	-		
LpMDHh55	:	-----		:	-		
LpMDHh56	:	-----		:	-		
LpMDHh57	:	-----		:	-		
LpMDHh58	:	-----		:	-		
LpMDHh59	:	-----		:	-		
LpMDHh60	:	-----		:	-		
LpMDHh61	:	-----		:	-		
LpMDHh62	:	-----		:	-		
LpMDHh63	:	-----		:	-		
LpMDHh64	:	-----		:	-		

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

	640	*	660	*	680
LpMDHh1 :	GATCTCTGAGAGACTTGATGTC	CCAAGTTAGT	GATGTGAANAATGTTATCATCTGGGGCAATC	:	680
LpMDHh2 :	-----			:	-
LpMDHh3 :	-----			:	-
LpMDHh4 :	-----			:	-
LpMDHh5 :	GATCTCTGAGAGACTTGATGTC	CCAAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	640
LpMDHh6 :	GATCTCTGAGAGACTTGATGTC	CCAAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	638
LpMDHh7 :	GATCTCTGAGAGACTTGATGTC	CAAATTAGT	GATGTGAANAATGTTATCATCTGGGGCAATC	:	636
LpMDHh8 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	639
LpMDHh9 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	639
LpMDHh10 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	63
LpMDHh11 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	638
LpMDHh12 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	636
LpMDHh13 :	-----			:	-
LpMDHh14 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	636
LpMDHh15 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	636
LpMDHh16 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	636
LpMDHh17 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	635
LpMDHh18 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	636
LpMDHh19 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	636
LpMDHh20 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	635
LpMDHh21 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	636
LpMDHh22 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	636
LpMDHh23 :	-----			:	-
LpMDHh24 :	-----			:	-
LpMDHh25 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAANAATGTTATCATCTGGGGCAATC	:	635
LpMDHh26 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAANAATGTTATCATCTGGGGCAATC	:	634
LpMDHh27 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	635
LpMDHh28 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	633
LpMDHh29 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	633
LpMDHh30 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	634
LpMDHh31 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	595
LpMDHh32 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAANAATGTTATCATCTGGGGCAATC	:	634
LpMDHh34 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	633
LpMDHh35 :	-----			:	-
LpMDHh36 :	GATCTCTGANAGACCTTGATGTCC	AAGTTA-----		:	599
LpMDHh37 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATG-----	:	606
LpMDHh38 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	631
LpMDHh39 :	-----			:	-
LpMDHh40 :	-----			:	-
LpMDHh41 :	GANCTCTGAGAGACNTGATGC	CCAAGNTNGNNTGN-----		:	605
LpMDHh42 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	630
LpMDHh43 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	631
LpMDHh44 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	630
LpMDHh45 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	629
LpMDHh46 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	630
LpMDHh47 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAANAATGTTATCATCTGGGGCAATC	:	627
LpMDHh48 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	623
LpMDHh49 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	626
LpMDHh50 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	604
LpMDHh51 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	587
LpMDHh52 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	553
LpMDHh53 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAANAATGTTATCATCTGGGGCAATC	:	475
LpMDHh54 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	304
LpMDHh55 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	226
LpMDHh56 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	206
LpMDHh57 :	GATCTCTGAGAGACTTGATGTCC	AAGTTAGT	GATGTGAAGAATGTTATCATCTGGGGCAATC	:	202
LpMDHh58 :	-----		GCAATC	:	6
LpMDHh59 :	-----			:	-
LpMDHh60 :	-----			:	-
LpMDHh61 :	-----			:	-
LpMDHh62 :	-----			:	-
LpMDHh6					

LpMDHh1 : ACTCTTTCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 742
LpMDHh2 : ----- : -
LpMDHh3 : ----- : -
LpMDHh4 : ----- : -
LpMDHh5 : ACTCTTCCAGT----- : 650
LpMDHh6 : ACTCTTCCAGTCAGTACCCTGA----- : 660
LpMDHh7 : ACCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 693
LpMDHh8 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 701
LpMDHh9 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 701
LpMDHh10 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 684
LpMDHh11 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 700
LpMDHh12 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 698
LpMDHh13 : ----- : -
LpMDHh14 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 692
LpMDHh15 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 698
LpMDHh16 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 698
LpMDHh17 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 697
LpMDHh18 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 698
LpMDHh19 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 698
LpMDHh20 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 697
LpMDHh21 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 698
LpMDHh22 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 698
LpMDHh23 : ----- : -
LpMDHh24 : ----- : -
LpMDHh25 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 696
LpMDHh26 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 646
LpMDHh27 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 697
LpMDHh28 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 695
LpMDHh29 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 695
LpMDHh30 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 696
LpMDHh31 : ----- : -
LpMDHh32 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 696
LpMDHh33 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 695
LpMDHh34 : ----- : -
LpMDHh35 : ----- : -
LpMDHh36 : ----- : -
LpMDHh37 : ----- : -
LpMDHh38 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 686
LpMDHh39 : ----- : -
LpMDHh40 : ----- : -
LpMDHh41 : ----- : -
LpMDHh42 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 685
LpMDHh43 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 693
LpMDHh44 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 692
LpMDHh45 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 690
LpMDHh46 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 692
LpMDHh47 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 679
LpMDHh48 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 676
LpMDHh49 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 688
LpMDHh50 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 666
LpMDHh51 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 649
LpMDHh52 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 615
LpMDHh53 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 513
LpMDHh54 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 366
LpMDHh55 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 288
LpMDHh56 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 268
LpMDHh57 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 264
LpMDHh58 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 67
LpMDHh59 : ----- : 49
LpMDHh60 : ----- : 14
LpMDHh61 : ----- : 8
LpMDHh62 : ----- : -
LpMDHh63 : ----- : -
LpMDHh64 : ----- : -

	*	760	*	780	*	800	
LpMDHh1	:	CCTGTTTCGCGAACTTGT	TAAAGACGATG	---	---	---	770
LpMDHh2	:	---	---	---	---	---	-
LpMDHh3	:	---	---	---	---	---	-
LpMDHh4	:	---	---	---	---	---	-
LpMDHh5	:	---	---	---	---	---	-
LpMDHh6	:	---	---	---	---	---	-
LpMDHh7	:	---	---	---	---	---	-
LpMDHh8	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	763
LpMDHh9	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	763
LpMDHh10	:	---	---	---	---	---	-
LpMDHh11	:	CCTGTTTC	---	---	---	---	707
LpMDHh12	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	760
LpMDHh13	:	---	---	---	---	---	-
LpMDHh14	:	---	---	---	---	---	-
LpMDHh15	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	760
LpMDHh16	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	760
LpMDHh17	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	759
LpMDHh18	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	760
LpMDHh19	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	760
LpMDHh20	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	759
LpMDHh21	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	760
LpMDHh22	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	760
LpMDHh23	:	---	---	---	---	---	-
LpMDHh24	:	---	---	---	---	---	-
LpMDHh25	:	---	---	---	---	---	-
LpMDHh26	:	---	---	---	---	---	-
LpMDHh27	:	CCTGTTTCGCGAACT	---	---	---	---	711
LpMDHh28	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	757
LpMDHh29	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	757
LpMDHh30	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	758
LpMDHh31	:	---	---	---	---	---	-
LpMDHh32	:	---	---	---	---	---	-
LpMDHh34	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	757
LpMDHh35	:	---	---	---	---	---	-
LpMDHh36	:	---	---	---	---	---	-
LpMDHh37	:	---	---	---	---	---	-
LpMDHh38	:	---	---	---	---	---	-
LpMDHh39	:	---	---	---	---	---	-
LpMDHh40	:	---	---	---	---	---	-
LpMDHh41	:	---	---	---	---	---	-
LpMDHh42	:	---	---	---	---	---	-
LpMDHh43	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	755
LpMDHh44	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	754
LpMDHh45	:	---	---	---	---	---	-
LpMDHh46	:	CCTGTTTCG	---	---	---	---	700
LpMDHh47	:	---	---	---	---	---	-
LpMDHh48	:	---	---	---	---	---	-
LpMDHh49	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	750
LpMDHh50	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	728
LpMDHh51	:	CCTGTTTCGCGAACTTGT	TAAAGACGAT	---	---	---	676
LpMDHh52	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	677
LpMDHh53	:	---	---	---	---	---	-
LpMDHh54	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	428
LpMDHh55	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	350
LpMDHh56	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	330
LpMDHh57	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	326
LpMDHh58	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	129
LpMDHh59	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	111
LpMDHh60	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	75
LpMDHh61	:	CCTGTTTCGCGAACTTGT	TAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA	:	---	---	70
LpMDHh62	:	---	---	---	---	---	-
LpMDHh63	:	---	---	---	---	---	-
LpMDHh64	:	---	---	---	---	---	-

	*	820	*	840	*	860	
LpMDHh1	:	-----		-----		-----	-
LpMDHh2	:	-----		-----		-----	-
LpMDHh3	:	-----		-----		-----	-
LpMDHh4	:	-----		-----		-----	-
LpMDHh5	:	-----		-----		-----	-
LpMDHh6	:	-----		-----		-----	-
LpMDHh7	:	-----		-----		-----	-
LpMDHh8	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAG		-----		-----	793
LpMDHh9	:	GCAGCGTGGTGCTGCAATCATCAAAGGAGGAAG		-----		-----	797
LpMDHh10	:	-----		-----		-----	-
LpMDHh11	:	-----		-----		-----	-
LpMDHh12	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTTCA		-----		-----	801
LpMDHh13	:	-----		-----		-----	-
LpMDHh14	:	-----		-----		-----	-
LpMDHh15	:	GCAG		-----		-----	764
LpMDHh16	:	GCAGCGTGG		-----		-----	769
LpMDHh17	:	GCAGCGTGGTG		-----		-----	770
LpMDHh18	:	GCAGCGTGGTGCTGCAATC		-----		-----	779
LpMDHh19	:	GCAGCGTGGTGCTGCAATCATCAAAGCG		-----		-----	788
LpMDHh20	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGC		-----		-----	794
LpMDHh21	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTT		-----		-----	797
LpMDHh22	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTTCAAGT		-----		-----	802
LpMDHh23	:	-----		-----		-----	-
LpMDHh24	:	-----		-----		-----	-
LpMDHh25	:	-----		-----		-----	-
LpMDHh26	:	-----		-----		-----	-
LpMDHh27	:	-----		-----		-----	-
LpMDHh28	:	GCAGCGTGGTG		-----		-----	768
LpMDHh29	:	GCAGCGTGGTGCTGCAATCATCAAAG		-----		-----	783
LpMDHh30	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTTCAAGTGC		-----		-----	803
LpMDHh31	:	-----		-----		-----	-
LpMDHh32	:	-----		-----		-----	-
LpMDHh34	:	GCAGCGTGGTGCTGCAATCAT		-----		-----	779
LpMDHh35	:	-----		-----		-----	-
LpMDHh36	:	-----		-----		-----	-
LpMDHh37	:	-----		-----		-----	-
LpMDHh38	:	-----		-----		-----	-
LpMDHh39	:	-----		-----		-----	-
LpMDHh40	:	-----		-----		-----	-
LpMDHh41	:	-----		-----		-----	-
LpMDHh42	:	-----		-----		-----	-
LpMDHh43	:	GCAGCGTG		-----		-----	763
LpMDHh44	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCT		-----		-----	790
LpMDHh45	:	-----		-----		-----	-
LpMDHh46	:	-----		-----		-----	-
LpMDHh47	:	-----		-----		-----	-
LpMDHh48	:	-----		-----		-----	-
LpMDHh49	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCT		-----		-----	786
LpMDHh50	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTG		-----		-----	772
LpMDHh51	:	-----		-----		-----	-
LpMDHh52	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT		-----		-----	739
LpMDHh53	:	-----		-----		-----	-
LpMDHh54	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT		-----		-----	490
LpMDHh55	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT		-----		-----	412
LpMDHh56	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT		-----		-----	392
LpMDHh57	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT		-----		-----	388
LpMDHh58	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT		-----		-----	191
LpMDHh59	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT		-----		-----	173
LpMDHh60	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT		-----		-----	137
LpMDHh61	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT		-----		-----	132
LpMDHh62	:	-----		-----		-----	-
LpMDHh63	:	-----		-----		-----	-
LpMDHh64	:	-----		-----		-----	-

	*	880	*	900	*	920	*
LpMDHh1	:	-----					
LpMDHh2	:	-----					
LpMDHh3	:	-----					
LpMDHh4	:	-----					
LpMDHh5	:	-----					
LpMDHh6	:	-----					
LpMDHh7	:	-----					
LpMDHh8	:	-----					
LpMDHh9	:	-----					
LpMDHh10	:	-----					
LpMDHh11	:	-----					
LpMDHh12	:	-----					
LpMDHh13	:	-----					
LpMDHh14	:	-----					
LpMDHh15	:	-----					
LpMDHh16	:	-----					
LpMDHh17	:	-----					
LpMDHh18	:	-----					
LpMDHh19	:	-----					
LpMDHh20	:	-----					
LpMDHh21	:	-----					
LpMDHh22	:	-----					
LpMDHh23	:	-----					
LpMDHh24	:	-----					
LpMDHh25	:	-----					
LpMDHh26	:	-----					
LpMDHh27	:	-----					
LpMDHh28	:	-----					
LpMDHh29	:	-----					
LpMDHh30	:	-----					
LpMDHh31	:	-----					
LpMDHh32	:	-----					
LpMDHh34	:	-----					
LpMDHh35	:	-----					
LpMDHh36	:	-----					
LpMDHh37	:	-----					
LpMDHh38	:	-----					
LpMDHh39	:	-----					
LpMDHh40	:	-----					
LpMDHh41	:	-----					
LpMDHh42	:	-----					
LpMDHh43	:	-----					
LpMDHh44	:	-----					
LpMDHh45	:	-----					
LpMDHh46	:	-----					
LpMDHh47	:	-----					
LpMDHh48	:	-----					
LpMDHh49	:	-----					
LpMDHh50	:	-----					
LpMDHh51	:	-----					
LpMDHh52	:	CTGCTTGTGACCACATCCGTGATT					763
LpMDHh53	:	-----					
LpMDHh54	:	CTGCTTGTGACCACATCCGCGATTGGGTTCTCGGAACCCCTGAGGGAAACATTTGTTTCCATG					552
LpMDHh55	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGGAAACATTTGTTTCCATG					474
LpMDHh56	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGGAAACATTTGTTTCCATG					454
LpMDHh57	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGGAAACATTTGTTTCCATG					450
LpMDHh58	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGGAAACATTTGTTTCCATG					253
LpMDHh59	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGGAAACATTTGTTTCCATG					235
LpMDHh60	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGGAAACATTTGTTTCCATG					199
LpMDHh61	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGGAAACATTTGTTTCCATG					194
LpMDHh62	:	-----					
LpMDHh63	:	-----					
LpMDHh64	:	-----					



	940	*	960	*	980	*
LpMDHh1	:	-----				
LpMDHh2	:	-----				
LpMDHh3	:	-----				
LpMDHh4	:	-----				
LpMDHh5	:	-----				
LpMDHh6	:	-----				
LpMDHh7	:	-----				
LpMDHh8	:	-----				
LpMDHh9	:	-----				
LpMDHh10	:	-----				
LpMDHh11	:	-----				
LpMDHh12	:	-----				
LpMDHh13	:	-----				
LpMDHh14	:	-----				
LpMDHh15	:	-----				
LpMDHh16	:	-----				
LpMDHh17	:	-----				
LpMDHh18	:	-----				
LpMDHh19	:	-----				
LpMDHh20	:	-----				
LpMDHh21	:	-----				
LpMDHh22	:	-----				
LpMDHh23	:	-----				
LpMDHh24	:	-----				
LpMDHh25	:	-----				
LpMDHh26	:	-----				
LpMDHh27	:	-----				
LpMDHh28	:	-----				
LpMDHh29	:	-----				
LpMDHh30	:	-----				
LpMDHh31	:	-----				
LpMDHh32	:	-----				
LpMDHh34	:	-----				
LpMDHh35	:	-----				
LpMDHh36	:	-----				
LpMDHh37	:	-----				
LpMDHh38	:	-----				
LpMDHh39	:	-----				
LpMDHh40	:	-----				
LpMDHh41	:	-----				
LpMDHh42	:	-----				
LpMDHh43	:	-----				
LpMDHh44	:	-----				
LpMDHh45	:	-----				
LpMDHh46	:	-----				
LpMDHh47	:	-----				
LpMDHh48	:	-----				
LpMDHh49	:	-----				
LpMDHh50	:	-----				
LpMDHh51	:	-----				
LpMDHh52	:	-----				
LpMDHh53	:	-----				
LpMDHh54	:	GGTGTGTATTCTGATGGNT-ATACN	GGGTGCCTGCTGGGCTTATCTACTCCTT	CCAGTAAC		
LpMDHh55	:	GGTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTT	CCAGTAAC		613	
LpMDHh56	:	GGTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTT	CCAGTAAC		536	
LpMDHh57	:	GGTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTT	CCAGTAAC		516	
LpMDHh58	:	GGTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTT	CCAGTAAC		512	
LpMDHh59	:	GGTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTT	CCAGTAAC		315	
LpMDHh60	:	GGTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTT	CCAGTAAC		297	
LpMDHh61	:	GGTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTT	CCAGTAAC		261	
LpMDHh62	:	GGTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTT	CCAGTAAC		256	
LpMDHh63	:	-----				
LpMDHh64	:	-----				



	1000	*	1020	*	1040	*
LpMDHh1	:	-----	-----	-----	-----	-----
LpMDHh2	:	-----	-----	-----	-----	-----
LpMDHh3	:	-----	-----	-----	-----	-----
LpMDHh4	:	-----	-----	-----	-----	-----
LpMDHh5	:	-----	-----	-----	-----	-----
LpMDHh6	:	-----	-----	-----	-----	-----
LpMDHh7	:	-----	-----	-----	-----	-----
LpMDHh8	:	-----	-----	-----	-----	-----
LpMDHh9	:	-----	-----	-----	-----	-----
LpMDHh10	:	-----	-----	-----	-----	-----
LpMDHh11	:	-----	-----	-----	-----	-----
LpMDHh12	:	-----	-----	-----	-----	-----
LpMDHh13	:	-----	-----	-----	-----	-----
LpMDHh14	:	-----	-----	-----	-----	-----
LpMDHh15	:	-----	-----	-----	-----	-----
LpMDHh16	:	-----	-----	-----	-----	-----
LpMDHh17	:	-----	-----	-----	-----	-----
LpMDHh18	:	-----	-----	-----	-----	-----
LpMDHh19	:	-----	-----	-----	-----	-----
LpMDHh20	:	-----	-----	-----	-----	-----
LpMDHh21	:	-----	-----	-----	-----	-----
LpMDHh22	:	-----	-----	-----	-----	-----
LpMDHh23	:	-----	-----	-----	-----	-----
LpMDHh24	:	-----	-----	-----	-----	-----
LpMDHh25	:	-----	-----	-----	-----	-----
LpMDHh26	:	-----	-----	-----	-----	-----
LpMDHh27	:	-----	-----	-----	-----	-----
LpMDHh28	:	-----	-----	-----	-----	-----
LpMDHh29	:	-----	-----	-----	-----	-----
LpMDHh30	:	-----	-----	-----	-----	-----
LpMDHh31	:	-----	-----	-----	-----	-----
LpMDHh32	:	-----	-----	-----	-----	-----
LpMDHh34	:	-----	-----	-----	-----	-----
LpMDHh35	:	-----	-----	-----	-----	-----
LpMDHh36	:	-----	-----	-----	-----	-----
LpMDHh37	:	-----	-----	-----	-----	-----
LpMDHh38	:	-----	-----	-----	-----	-----
LpMDHh39	:	-----	-----	-----	-----	-----
LpMDHh40	:	-----	-----	-----	-----	-----
LpMDHh41	:	-----	-----	-----	-----	-----
LpMDHh42	:	-----	-----	-----	-----	-----
LpMDHh43	:	-----	-----	-----	-----	-----
LpMDHh44	:	-----	-----	-----	-----	-----
LpMDHh45	:	-----	-----	-----	-----	-----
LpMDHh46	:	-----	-----	-----	-----	-----
LpMDHh47	:	-----	-----	-----	-----	-----
LpMDHh48	:	-----	-----	-----	-----	-----
LpMDHh49	:	-----	-----	-----	-----	-----
LpMDHh50	:	-----	-----	-----	-----	-----
LpMDHh51	:	-----	-----	-----	-----	-----
LpMDHh52	:	-----	-----	-----	-----	-----
LpMDHh53	:	-----	-----	-----	-----	-----
LpMDHh54	:	TTGCTGNGGGGGGAATGGACAATTGTTCAAAAGGCTNCCNATCNACNAGTT	-----	-----	-----	664
LpMDHh55	:	TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA	-----	-----	-----	598
LpMDHh56	:	TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA	-----	-----	-----	578
LpMDHh57	:	TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA	-----	-----	-----	574
LpMDHh58	:	TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA	-----	-----	-----	377
LpMDHh59	:	TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA	-----	-----	-----	359
LpMDHh60	:	TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA	-----	-----	-----	323
LpMDHh61	:	TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA	-----	-----	-----	318
LpMDHh62	:	-----	CCATCCCGAAAGCCGAGTTCTC	-----	TTTATAG	28
LpMDHh63	:	-----	-----	-----	-----	-----
LpMDHh64	:	-----	-----	-----	-----	-----



	1060	*	1080	*	1100	*	
LpMDHh1	:	-	-	-	-	-	-
LpMDHh2	:	-	-	-	-	-	-
LpMDHh3	:	-	-	-	-	-	-
LpMDHh4	:	-	-	-	-	-	-
LpMDHh5	:	-	-	-	-	-	-
LpMDHh6	:	-	-	-	-	-	-
LpMDHh7	:	-	-	-	-	-	-
LpMDHh8	:	-	-	-	-	-	-
LpMDHh9	:	-	-	-	-	-	-
LpMDHh10	:	-	-	-	-	-	-
LpMDHh11	:	-	-	-	-	-	-
LpMDHh12	:	-	-	-	-	-	-
LpMDHh13	:	-	-	-	-	-	-
LpMDHh14	:	-	-	-	-	-	-
LpMDHh15	:	-	-	-	-	-	-
LpMDHh16	:	-	-	-	-	-	-
LpMDHh17	:	-	-	-	-	-	-
LpMDHh18	:	-	-	-	-	-	-
LpMDHh19	:	-	-	-	-	-	-
LpMDHh20	:	-	-	-	-	-	-
LpMDHh21	:	-	-	-	-	-	-
LpMDHh22	:	-	-	-	-	-	-
LpMDHh23	:	-	-	-	-	-	-
LpMDHh24	:	-	-	-	-	-	-
LpMDHh25	:	-	-	-	-	-	-
LpMDHh26	:	-	-	-	-	-	-
LpMDHh27	:	-	-	-	-	-	-
LpMDHh28	:	-	-	-	-	-	-
LpMDHh29	:	-	-	-	-	-	-
LpMDHh30	:	-	-	-	-	-	-
LpMDHh31	:	-	-	-	-	-	-
LpMDHh32	:	-	-	-	-	-	-
LpMDHh34	:	-	-	-	-	-	-
LpMDHh35	:	-	-	-	-	-	-
LpMDHh36	:	-	-	-	-	-	-
LpMDHh37	:	-	-	-	-	-	-
LpMDHh38	:	-	-	-	-	-	-
LpMDHh39	:	-	-	-	-	-	-
LpMDHh40	:	-	-	-	-	-	-
LpMDHh41	:	-	-	-	-	-	-
LpMDHh42	:	-	-	-	-	-	-
LpMDHh43	:	-	-	-	-	-	-
LpMDHh44	:	-	-	-	-	-	-
LpMDHh45	:	-	-	-	-	-	-
LpMDHh46	:	-	-	-	-	-	-
LpMDHh47	:	-	-	-	-	-	-
LpMDHh48	:	-	-	-	-	-	-
LpMDHh49	:	-	-	-	-	-	-
LpMDHh50	:	-	-	-	-	-	-
LpMDHh51	:	-	-	-	-	-	-
LpMDHh52	:	-	-	-	-	-	-
LpMDHh53	:	-	-	-	-	-	-
LpMDHh54	:	-	-	-	-	-	-
LpMDHh55	:	AGATGGATGCCACAGCCCAGGAGCTCTCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAG					660
LpMDHh56	:	AGATGGATGCCACAGCCCAGGAGCTCTCG ^N AGGAGAAGGCTCTCGCCTACTCGTGCCTCGAG					640
LpMDHh57	:	AGATGGATGCCACAGCCCAGGAGCTCTCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAG					636
LpMDHh58	:	AGATGGATGCCACAGCCCAGGAGCTCTCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAG					439
LpMDHh59	:	AGATGGATGCCACAGCCCAGGAGCTCTCGGAGGAGAAGGCTCT ^T GCCTACTCGTGCCTCGAG					421
LpMDHh60	:	AGATGGATGCCACAGCCCAGGAGCTCTCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAG					385
LpMDHh61	:	AGATGGATGCCACAGCCCAGGAGCTCTCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAG					380
LpMDHh62	:	AGA-GGA ^T GCCACAGCCCAGGAGCTCTCGGAGGAGAAGG ^T TCGCCTACTCG ^T GCCTCGAG					89
LpMDHh63	:	-	-	-	-	-	-
LpMDHh64	:	-	-	-	-	-	-



	1120	*	1140	*	1160	*	11	
LpMDHh1	:	-----	:	-----	:	-----	:	-
LpMDHh2	:	-----	:	-----	:	-----	:	-
LpMDHh3	:	-----	:	-----	:	-----	:	-
LpMDHh4	:	-----	:	-----	:	-----	:	-
LpMDHh5	:	-----	:	-----	:	-----	:	-
LpMDHh6	:	-----	:	-----	:	-----	:	-
LpMDHh7	:	-----	:	-----	:	-----	:	-
LpMDHh8	:	-----	:	-----	:	-----	:	-
LpMDHh9	:	-----	:	-----	:	-----	:	-
LpMDHh10	:	-----	:	-----	:	-----	:	-
LpMDHh11	:	-----	:	-----	:	-----	:	-
LpMDHh12	:	-----	:	-----	:	-----	:	-
LpMDHh13	:	-----	:	-----	:	-----	:	-
LpMDHh14	:	-----	:	-----	:	-----	:	-
LpMDHh15	:	-----	:	-----	:	-----	:	-
LpMDHh16	:	-----	:	-----	:	-----	:	-
LpMDHh17	:	-----	:	-----	:	-----	:	-
LpMDHh18	:	-----	:	-----	:	-----	:	-
LpMDHh19	:	-----	:	-----	:	-----	:	-
LpMDHh20	:	-----	:	-----	:	-----	:	-
LpMDHh21	:	-----	:	-----	:	-----	:	-
LpMDHh22	:	-----	:	-----	:	-----	:	-
LpMDHh23	:	-----	:	-----	:	-----	:	-
LpMDHh24	:	-----	:	-----	:	-----	:	-
LpMDHh25	:	-----	:	-----	:	-----	:	-
LpMDHh26	:	-----	:	-----	:	-----	:	-
LpMDHh27	:	-----	:	-----	:	-----	:	-
LpMDHh28	:	-----	:	-----	:	-----	:	-
LpMDHh29	:	-----	:	-----	:	-----	:	-
LpMDHh30	:	-----	:	-----	:	-----	:	-
LpMDHh31	:	-----	:	-----	:	-----	:	-
LpMDHh32	:	-----	:	-----	:	-----	:	-
LpMDHh34	:	-----	:	-----	:	-----	:	-
LpMDHh35	:	-----	:	-----	:	-----	:	-
LpMDHh36	:	-----	:	-----	:	-----	:	-
LpMDHh37	:	-----	:	-----	:	-----	:	-
LpMDHh38	:	-----	:	-----	:	-----	:	-
LpMDHh39	:	-----	:	-----	:	-----	:	-
LpMDHh40	:	-----	:	-----	:	-----	:	-
LpMDHh41	:	-----	:	-----	:	-----	:	-
LpMDHh42	:	-----	:	-----	:	-----	:	-
LpMDHh43	:	-----	:	-----	:	-----	:	-
LpMDHh44	:	-----	:	-----	:	-----	:	-
LpMDHh45	:	-----	:	-----	:	-----	:	-
LpMDHh46	:	-----	:	-----	:	-----	:	-
LpMDHh47	:	-----	:	-----	:	-----	:	-
LpMDHh48	:	-----	:	-----	:	-----	:	-
LpMDHh49	:	-----	:	-----	:	-----	:	-
LpMDHh50	:	-----	:	-----	:	-----	:	-
LpMDHh51	:	-----	:	-----	:	-----	:	-
LpMDHh52	:	-----	:	-----	:	-----	:	-
LpMDHh53	:	-----	:	-----	:	-----	:	-
LpMDHh54	:	-----	:	-----	:	-----	:	-
LpMDHh55	:	TA	ACTGC	ATA	CCAGG	GAGCAGCTGCCGCTCTGATGTTTTGAATAAAA	AGGAACATTTTGGCTC	722
LpMDHh56	:	TA	ACTGC	ATA	CCAGG	GAGCAGCTGCCGCTCTGATGTTTTGAATAAAA	AGGAACATTTTGGCTC	701
LpMDHh57	:	TA	ACTGC	ATA	CCAGG	GAGCAGCTGCCGCTCTGATGTTTTGAATAAAA	AGGAACATTTTGGCTC	667
LpMDHh58	:	TA	ACTGC	ATA	CCAGG	GAGCAGCTGCCGCTCTGATGTTTTGAATAAAA	AGGAACATTTTGGCTC	501
LpMDHh59	:	TA	ACTGC	ATA	CCAGG	GAGCAGCTGCCGCTCTGATGTTTTGAATAAAA	AGGAACATTTTGGCTC	483
LpMDHh60	:	TA	ACTGC	ATA	CCAGG	GAGCAGCTGCCGCTCTGATGTTTTGAATAAAA	AGGAACATTTTGGCTC	447
LpMDHh61	:	TA	ACTGC	ATA	CCAGG	GAGCAGCTGCCGCTCTGATGTTTTGAATAAAA	AGGAACATTTTGGCTC	442
LpMDHh62	:	TA	ACTGC	ATA	CCAGG	GAGCAGCTGCCGCTCTGATGTTTTGAATAAAA	AGGAACATTTTGGCTC	151
LpMDHh63	:	TA	ACTGC	ATA	CCAGG	GAGCAGCTGCCGCTCTGATGTTTTGAATAAAA	AGGAACATTTTGGCTC	100
LpMDHh64	:	-----	:	-----	:	-----	:	-



	80	*	1200	*	1220	*	1240	
LpMDHh1	:	-	-	-	-	-	-	-
LpMDHh2	:	-	-	-	-	-	-	-
LpMDHh3	:	-	-	-	-	-	-	-
LpMDHh4	:	-	-	-	-	-	-	-
LpMDHh5	:	-	-	-	-	-	-	-
LpMDHh6	:	-	-	-	-	-	-	-
LpMDHh7	:	-	-	-	-	-	-	-
LpMDHh8	:	-	-	-	-	-	-	-
LpMDHh9	:	-	-	-	-	-	-	-
LpMDHh10	:	-	-	-	-	-	-	-
LpMDHh11	:	-	-	-	-	-	-	-
LpMDHh12	:	-	-	-	-	-	-	-
LpMDHh13	:	-	-	-	-	-	-	-
LpMDHh14	:	-	-	-	-	-	-	-
LpMDHh15	:	-	-	-	-	-	-	-
LpMDHh16	:	-	-	-	-	-	-	-
LpMDHh17	:	-	-	-	-	-	-	-
LpMDHh18	:	-	-	-	-	-	-	-
LpMDHh19	:	-	-	-	-	-	-	-
LpMDHh20	:	-	-	-	-	-	-	-
LpMDHh21	:	-	-	-	-	-	-	-
LpMDHh22	:	-	-	-	-	-	-	-
LpMDHh23	:	-	-	-	-	-	-	-
LpMDHh24	:	-	-	-	-	-	-	-
LpMDHh25	:	-	-	-	-	-	-	-
LpMDHh26	:	-	-	-	-	-	-	-
LpMDHh27	:	-	-	-	-	-	-	-
LpMDHh28	:	-	-	-	-	-	-	-
LpMDHh29	:	-	-	-	-	-	-	-
LpMDHh30	:	-	-	-	-	-	-	-
LpMDHh31	:	-	-	-	-	-	-	-
LpMDHh32	:	-	-	-	-	-	-	-
LpMDHh34	:	-	-	-	-	-	-	-
LpMDHh35	:	-	-	-	-	-	-	-
LpMDHh36	:	-	-	-	-	-	-	-
LpMDHh37	:	-	-	-	-	-	-	-
LpMDHh38	:	-	-	-	-	-	-	-
LpMDHh39	:	-	-	-	-	-	-	-
LpMDHh40	:	-	-	-	-	-	-	-
LpMDHh41	:	-	-	-	-	-	-	-
LpMDHh42	:	-	-	-	-	-	-	-
LpMDHh43	:	-	-	-	-	-	-	-
LpMDHh44	:	-	-	-	-	-	-	-
LpMDHh45	:	-	-	-	-	-	-	-
LpMDHh46	:	-	-	-	-	-	-	-
LpMDHh47	:	-	-	-	-	-	-	-
LpMDHh48	:	-	-	-	-	-	-	-
LpMDHh49	:	-	-	-	-	-	-	-
LpMDHh50	:	-	-	-	-	-	-	-
LpMDHh51	:	-	-	-	-	-	-	-
LpMDHh52	:	-	-	-	-	-	-	-
LpMDHh53	:	-	-	-	-	-	-	-
LpMDHh54	:	-	-	-	-	-	-	-
LpMDHh55	:	CATGAAACTCAT	-	-	-	-	-	734
LpMDHh56	:	CATG	-	-	-	-	-	705
LpMDHh57	:	-	-	-	-	-	-	-
LpMDHh58	:	CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAG	-	-	-	-	-	563
LpMDHh59	:	CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAG	-	-	-	-	-	545
LpMDHh60	:	CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAG	-	-	-	-	-	509
LpMDHh61	:	CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAG	-	-	-	-	-	504
LpMDHh62	:	CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAG	-	-	-	-	-	213
LpMDHh63	:	CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAG	-	-	-	-	-	162
LpMDHh64	:	-	-	-	-	-	-	-

* 1260

* 1280

* 1300

LpMDHh1	:	-----	:	-
LpMDHh2	:	-----	:	-
LpMDHh3	:	-----	:	-
LpMDHh4	:	-----	:	-
LpMDHh5	:	-----	:	-
LpMDHh6	:	-----	:	-
LpMDHh7	:	-----	:	-
LpMDHh8	:	-----	:	-
LpMDHh9	:	-----	:	-
LpMDHh10	:	-----	:	-
LpMDHh11	:	-----	:	-
LpMDHh12	:	-----	:	-
LpMDHh13	:	-----	:	-
LpMDHh14	:	-----	:	-
LpMDHh15	:	-----	:	-
LpMDHh16	:	-----	:	-
LpMDHh17	:	-----	:	-
LpMDHh18	:	-----	:	-
LpMDHh19	:	-----	:	-
LpMDHh20	:	-----	:	-
LpMDHh21	:	-----	:	-
LpMDHh22	:	-----	:	-
LpMDHh23	:	-----	:	-
LpMDHh24	:	-----	:	-
LpMDHh25	:	-----	:	-
LpMDHh26	:	-----	:	-
LpMDHh27	:	-----	:	-
LpMDHh28	:	-----	:	-
LpMDHh29	:	-----	:	-
LpMDHh30	:	-----	:	-
LpMDHh31	:	-----	:	-
LpMDHh32	:	-----	:	-
LpMDHh34	:	-----	:	-
LpMDHh35	:	-----	:	-
LpMDHh36	:	-----	:	-
LpMDHh37	:	-----	:	-
LpMDHh38	:	-----	:	-
LpMDHh39	:	-----	:	-
LpMDHh40	:	-----	:	-
LpMDHh41	:	-----	:	-
LpMDHh42	:	-----	:	-
LpMDHh43	:	-----	:	-
LpMDHh44	:	-----	:	-
LpMDHh45	:	-----	:	-
LpMDHh46	:	-----	:	-
LpMDHh47	:	-----	:	-
LpMDHh48	:	-----	:	-
LpMDHh49	:	-----	:	-
LpMDHh50	:	-----	:	-
LpMDHh51	:	-----	:	-
LpMDHh52	:	-----	:	-
LpMDHh53	:	-----	:	-
LpMDHh54	:	-----	:	-
LpMDHh55	:	-----	:	-
LpMDHh56	:	-----	:	-
LpMDHh57	:	-----	:	-
LpMDHh58	:	TGTGTATGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTG	:	625
LpMDHh59	:	TGTGTATGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTG	:	607
LpMDHh60	:	TGTGTATGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTG	:	571
LpMDHh61	:	TGTGTATGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTG	:	566
LpMDHh62	:	TGTGTATGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTG	:	275
LpMDHh63	:	TGTGTATGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTG	:	224
LpMDHh64	:	-----GNAAGNAGCTTTTGTAGCTCTATTTTCGCCTGNAAGATTTACAGGACAGGATATTG	:	55

* 1320 * 1340 * 1360

LpMDHh1	:	-----	:	-
LpMDHh2	:	-----	:	-
LpMDHh3	:	-----	:	-
LpMDHh4	:	-----	:	-
LpMDHh5	:	-----	:	-
LpMDHh6	:	-----	:	-
LpMDHh7	:	-----	:	-
LpMDHh8	:	-----	:	-
LpMDHh9	:	-----	:	-
LpMDHh10	:	-----	:	-
LpMDHh11	:	-----	:	-
LpMDHh12	:	-----	:	-
LpMDHh13	:	-----	:	-
LpMDHh14	:	-----	:	-
LpMDHh15	:	-----	:	-
LpMDHh16	:	-----	:	-
LpMDHh17	:	-----	:	-
LpMDHh18	:	-----	:	-
LpMDHh19	:	-----	:	-
LpMDHh20	:	-----	:	-
LpMDHh21	:	-----	:	-
LpMDHh22	:	-----	:	-
LpMDHh23	:	-----	:	-
LpMDHh24	:	-----	:	-
LpMDHh25	:	-----	:	-
LpMDHh26	:	-----	:	-
LpMDHh27	:	-----	:	-
LpMDHh28	:	-----	:	-
LpMDHh29	:	-----	:	-
LpMDHh30	:	-----	:	-
LpMDHh31	:	-----	:	-
LpMDHh32	:	-----	:	-
LpMDHh34	:	-----	:	-
LpMDHh35	:	-----	:	-
LpMDHh36	:	-----	:	-
LpMDHh37	:	-----	:	-
LpMDHh38	:	-----	:	-
LpMDHh39	:	-----	:	-
LpMDHh40	:	-----	:	-
LpMDHh41	:	-----	:	-
LpMDHh42	:	-----	:	-
LpMDHh43	:	-----	:	-
LpMDHh44	:	-----	:	-
LpMDHh45	:	-----	:	-
LpMDHh46	:	-----	:	-
LpMDHh47	:	-----	:	-
LpMDHh48	:	-----	:	-
LpMDHh49	:	-----	:	-
LpMDHh50	:	-----	:	-
LpMDHh51	:	-----	:	-
LpMDHh52	:	-----	:	-
LpMDHh53	:	-----	:	-
LpMDHh54	:	-----	:	-
LpMDHh55	:	-----	:	-
LpMDHh56	:	-----	:	-
LpMDHh57	:	-----	:	-
LpMDHh58	:	GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCAACCTCTTATTATTCCCGTGTGTA	:	687
LpMDHh59	:	GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCA-----	:	646
LpMDHh60	:	GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCAACCTCTTATTATTCCCTGTGTGTA	:	633
LpMDHh61	:	GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCAACCTCTTATTA-----	:	616
LpMDHh62	:	GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCAACCTCTTATTATTCCCTGTGTGTA	:	337
LpMDHh63	:	GCAGGAAGATTGGAACAATTTGACGTCTGACAAAAAATAA-----	:	265
LpMDHh64	:	GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCAACCTCTTA-TATTCCCTGTGTGTA	:	116

	*	1380	*	1400	*	1420	
LpMDHh1	:	-----	:	-----	:	-----	:
LpMDHh2	:	-----	:	-----	:	-----	:
LpMDHh3	:	-----	:	-----	:	-----	:
LpMDHh4	:	-----	:	-----	:	-----	:
LpMDHh5	:	-----	:	-----	:	-----	:
LpMDHh6	:	-----	:	-----	:	-----	:
LpMDHh7	:	-----	:	-----	:	-----	:
LpMDHh8	:	-----	:	-----	:	-----	:
LpMDHh9	:	-----	:	-----	:	-----	:
LpMDHh10	:	-----	:	-----	:	-----	:
LpMDHh11	:	-----	:	-----	:	-----	:
LpMDHh12	:	-----	:	-----	:	-----	:
LpMDHh13	:	-----	:	-----	:	-----	:
LpMDHh14	:	-----	:	-----	:	-----	:
LpMDHh15	:	-----	:	-----	:	-----	:
LpMDHh16	:	-----	:	-----	:	-----	:
LpMDHh17	:	-----	:	-----	:	-----	:
LpMDHh18	:	-----	:	-----	:	-----	:
LpMDHh19	:	-----	:	-----	:	-----	:
LpMDHh20	:	-----	:	-----	:	-----	:
LpMDHh21	:	-----	:	-----	:	-----	:
LpMDHh22	:	-----	:	-----	:	-----	:
LpMDHh23	:	-----	:	-----	:	-----	:
LpMDHh24	:	-----	:	-----	:	-----	:
LpMDHh25	:	-----	:	-----	:	-----	:
LpMDHh26	:	-----	:	-----	:	-----	:
LpMDHh27	:	-----	:	-----	:	-----	:
LpMDHh28	:	-----	:	-----	:	-----	:
LpMDHh29	:	-----	:	-----	:	-----	:
LpMDHh30	:	-----	:	-----	:	-----	:
LpMDHh31	:	-----	:	-----	:	-----	:
LpMDHh32	:	-----	:	-----	:	-----	:
LpMDHh34	:	-----	:	-----	:	-----	:
LpMDHh35	:	-----	:	-----	:	-----	:
LpMDHh36	:	-----	:	-----	:	-----	:
LpMDHh37	:	-----	:	-----	:	-----	:
LpMDHh38	:	-----	:	-----	:	-----	:
LpMDHh39	:	-----	:	-----	:	-----	:
LpMDHh40	:	-----	:	-----	:	-----	:
LpMDHh41	:	-----	:	-----	:	-----	:
LpMDHh42	:	-----	:	-----	:	-----	:
LpMDHh43	:	-----	:	-----	:	-----	:
LpMDHh44	:	-----	:	-----	:	-----	:
LpMDHh45	:	-----	:	-----	:	-----	:
LpMDHh46	:	-----	:	-----	:	-----	:
LpMDHh47	:	-----	:	-----	:	-----	:
LpMDHh48	:	-----	:	-----	:	-----	:
LpMDHh49	:	-----	:	-----	:	-----	:
LpMDHh50	:	-----	:	-----	:	-----	:
LpMDHh51	:	-----	:	-----	:	-----	:
LpMDHh52	:	-----	:	-----	:	-----	:
LpMDHh53	:	-----	:	-----	:	-----	:
LpMDHh54	:	-----	:	-----	:	-----	:
LpMDHh55	:	-----	:	-----	:	-----	:
LpMDHh56	:	-----	:	-----	:	-----	:
LpMDHh57	:	-----	:	-----	:	-----	:
LpMDHh58	:	TGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGCCATGATATTGGCAGG	:	-----	:	-----	748
LpMDHh59	:	-----	:	-----	:	-----	:
LpMDHh60	:	TGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGCCATGATATTGGCAGGA	:	-----	:	-----	695
LpMDHh61	:	-----	:	-----	:	-----	:
LpMDHh62	:	TGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGCCATGATATTGGCAGGA	:	-----	:	-----	399
LpMDHh63	:	-----	:	-----	:	-----	:
LpMDHh64	:	TGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGCCAGGATATTGGCAGGA	:	-----	:	-----	178

	* 1440 *	1460	* 1480	
LpMDHh1	:	-----	:	-
LpMDHh2	:	-----	:	-
LpMDHh3	:	-----	:	-
LpMDHh4	:	-----	:	-
LpMDHh5	:	-----	:	-
LpMDHh6	:	-----	:	-
LpMDHh7	:	-----	:	-
LpMDHh8	:	-----	:	-
LpMDHh9	:	-----	:	-
LpMDHh10	:	-----	:	-
LpMDHh11	:	-----	:	-
LpMDHh12	:	-----	:	-
LpMDHh13	:	-----	:	-
LpMDHh14	:	-----	:	-
LpMDHh15	:	-----	:	-
LpMDHh16	:	-----	:	-
LpMDHh17	:	-----	:	-
LpMDHh18	:	-----	:	-
LpMDHh19	:	-----	:	-
LpMDHh20	:	-----	:	-
LpMDHh21	:	-----	:	-
LpMDHh22	:	-----	:	-
LpMDHh23	:	-----	:	-
LpMDHh24	:	-----	:	-
LpMDHh25	:	-----	:	-
LpMDHh26	:	-----	:	-
LpMDHh27	:	-----	:	-
LpMDHh28	:	-----	:	-
LpMDHh29	:	-----	:	-
LpMDHh30	:	-----	:	-
LpMDHh31	:	-----	:	-
LpMDHh32	:	-----	:	-
LpMDHh34	:	-----	:	-
LpMDHh35	:	-----	:	-
LpMDHh36	:	-----	:	-
LpMDHh37	:	-----	:	-
LpMDHh38	:	-----	:	-
LpMDHh39	:	-----	:	-
LpMDHh40	:	-----	:	-
LpMDHh41	:	-----	:	-
LpMDHh42	:	-----	:	-
LpMDHh43	:	-----	:	-
LpMDHh44	:	-----	:	-
LpMDHh45	:	-----	:	-
LpMDHh46	:	-----	:	-
LpMDHh47	:	-----	:	-
LpMDHh48	:	-----	:	-
LpMDHh49	:	-----	:	-
LpMDHh50	:	-----	:	-
LpMDHh51	:	-----	:	-
LpMDHh52	:	-----	:	-
LpMDHh53	:	-----	:	-
LpMDHh54	:	-----	:	-
LpMDHh55	:	-----	:	-
LpMDHh56	:	-----	:	-
LpMDHh57	:	-----	:	-
LpMDHh58	:	-----	:	-
LpMDHh59	:	-----	:	-
LpMDHh60	:	GGATTGGAACAATTTGACGCCTGATTAAAACCAACCTCTTATTACTAAAAAAAAA	:	750
LpMDHh61	:	-----	:	-
LpMDHh62	:	GGATTGGAACAANNANANN	:	418
LpMDHh63	:	-----	:	-
LpMDHh64	:	GGATTGGAACAATTTGACGCCTGATTAAAACCAACCTCTTATTACTAAAAAAAAA	:	236

Figure 31 Nucleotide sequence of LpMDHi

LpMDHi : GTNCATAAAGCTGCCCAAAGCAATNCGTGNAATATTATCAGTAACCCTGTCAATTCTACC : 60

LpMDHi : GTACCAATTGCTGCTGAAGTATTTAAAAAAGCTGGGACATACAATNCTAAGAGATTGTTG : 120

LpMDHi : GGGGTTGACAACNGTTNGATGNNANTGACAGACCNTGCTCTTNGNNGNCGAGGTNCN : 177

Figure 32 Deduced amino acid sequence of LpMDHi

LpMDHi : XHKAAQSNXXNIISNPVNSTVPAAEVFKKAGTYNXKRLLGVDNXXMXXTDXALXXRG : 58

Figure 33 Nucleotide sequence of LpMDHj

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      *           20           *           40           *           60
LpMDHj : ANAAAGGAGCCGACGCAGGGGCGCAGAATTCCATCTGCTNACTCTGCCACCACCCAAGTT : 60

      *           80           *           100          *           120
LpMDHj : GGACATGGCGTCAGCTGTTACAATCAGTTCAGTCAGCGCGCAGGCCGCTTTGGTTTCAAA : 120

      *           140          *           160           *           180
LpMDHj : ACCAAGGAACCATGGCAGCACGAGCTACAGTGGCCTAAAGGCATCATCGTCGTCGATCAG : 180

      *           200          *           220           *           240
LpMDHj : CTTCTGAATCAGGAACATCATTCCTGGGCAAGACCGCCTCCCTCCGGGCAACTGTTACCAC : 240

      *           260          *           280           *           300
LpMDHj : AAGGGTTGTGCCAAAGGCGAAGTCTGGGTTCGCAGATATCGCCTCAGGCATCTTACAAGGT : 300

      *           320          *           340           *           360
LpMDHj : GGCGGTGCTTGGTGCTGCTGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAGATGTC : 360

      *           380          *           400           *           420
LpMDHj : TCCTCTGGTCTCGGAGCTGCGCCTGTATGATATCGCGAATGTCAAGGGCGTCGCTGCAGA : 420

      *           440          *           460           *           480
LpMDHj : TCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCAGAGCTAGC : 480

      *           500          *           520           *           540
LpMDHj : AGAGTGCTTGAAAGGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAGCCAGG : 540

      *           560          *           580           *           600
LpMDHj : CATGACCCGTGATGACCTTTTTTAACATNAATGCGGGAATCGNCAAGTCGCTTATTGAGGC : 600

      *           620          *           640           *           660
LpMDHj : TGTTCAGACAATTGCCCTGAGGGCCTTATTCATATCATCAACAACCCCGGTCAAACCTCC : 660

LpMDHj : CCCT : 664

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Figure 34 Deduced amino acid sequence of LpMDHj

LpMDHj : XRSRRRGAEFHLXTLPPPKLDMASAVTISSVSAQAALVSKPRNHGSTSYSGLKASSSSIS : 60

LpMDHj : FESGTSFLGKTASLRATVTTRVVPKAKSGSQISPQASYKVAVLGAAGGIGQPLGLLIKMS : 120

LpMDHj : PLVSELRLYDIANVKGVAADLSHCNTPAQVMDFTGPAELAECLKGVDVVVIPAGVPRKPG : 180

LpMDHj : MTRDDLFXNAGIXKSLIEAVADNCPEGLIHIINNPGQTPP : 221

are 35 Consensus contig nucleotide sequence of LpMDHk

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*           20           *           40           *           60
LpMDHk : TTTTTANCCCNCCAANTATCCAGNANCCACCTGGCCCTACACANAANAAAAACAAAAANN : 60

*           80           *           100          *           120
LpMDHk : AACCAGNACGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 120

*           140          *           160          *           180
LpMDHk : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 180

*           200          *           220          *           240
LpMDHk : TCGAAACCAAGGAATCATGGCAGCACAAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 240

*           260          *           280          *           300
LpMDHk : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 300

*           320          *           340          *           360
LpMDHk : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 360

*           380          *           400          *           420
LpMDHk : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 420

*           440          *           460          *           480
LpMDHk : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 480

*           500          *           520          *           540
LpMDHk : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCAATGGACTTCACTGGCCCAGCAGAA : 540

*           560          *           580          *           600
LpMDHk : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 600

*           620          *           640          *           660
LpMDHk : CCAGGCATGACCCGTGATGACCTTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 660

*           680          *           700          *           720
LpMDHk : GAGGCTGTTGCAGACAACCTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 720

*           740          *           760          *           780
LpMDHk : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 780

*           800          *           820          *           840
LpMDHk : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAGAAGAAG : 840

*           860          *           880          *           900
LpMDHk : AACCTCAGCCTCATCGATGTTGATGTCCCAGTTGTGCGTGGCCATGCTGGGATCACGATT : 900

*           920          *           940          *           960
LpMDHk : CTGCCTCTGTTGTCCAAGACTAGGCCCTTCTGTCAGCTTCACGGACGAGGAACTGAACAG : 960

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* 980 * 1000 * 1020
LpMDHk : CTGACAAAGAGGATACAGAACGCTGGGACAGAGGCGGTGGAGGCGAAGGCTGGTGCTGGC : 1020

* 1040 * 1060 * 1080
LpMDHk : TCTGCTACTCTGTCCATGGCTTATGCCGCTGCCAGATTGTGAGTCATCGCTCCGCGCA : 1080

* 1100 * 1120 * 1140
LpMDHk : ATGGCTGGTGATCCAGATGTTTACGAGTGCACGTATGTTTCAGTCTGAGTTAACAGAGCTT : 1140

* 1160 * 1180 * 1200
LpMDHk : CCATTCTTCGCGTCCAGAGTTAAGCTTGGGAAGGACGGNGTTGAGTCCATCATTTCCTCC : 1200

* 1220 * 1240 * 1260
LpMDHk : GACCTGGAGGGAGTGACGGAGTACGAGGCCAAGGCGCTTGANGCATTGAAGGCTGAGCTG : 1260

LpMDHk : AAG : 1263

are 36 Deduced amino acid sequence of LpMDHk

LpMDHk : XLXXQXSXXHLALHXXKTKXNQXARGEPPGRTQQFPKLEMASAVTISSVSAQAALV : 60

LpMDHk : SKPRNHGSTSYSGLKASSSSISFESGTSFLGKTASLRATITSRIVPKAKSGSQISPQASY : 120

LpMDHk : KVAVLGAAGGIGQPLGLLIKMSPLVSELRLYDIANVKGVAADLSHCNTPSQVMDFTGPÆ : 180

LpMDHk : LADCLKGVDVVVIPAGVPRKPGMTRDDLFNINAGIVKSLIEAVADNCPEAFIHIISNPVN : 240

LpMDHk : STVPIAAEILKQKGVYNPKLFGVSTLDVVRANTFVAQKKNLSDVDVPVVGGHAGITI : 300

LpMDHk : LPLLSKTRPSVSFTDEETEQLTKRIQNAGTEAVEAKAGAGSATLSMAYAAARFVESSLRA : 360

LpMDHk : MAGDPDVYECTYVQSELTLPFFASRVKLGKDXVESIISDLEGVTEYEAKALXALKÆL : 420

LpMDHk : K : 421

•

		20	*	40	*	60		
LpMDHk1	:	TNTTTANCCCNCCAANTATCCAGNANCCACCTG	CCCCAA	CCA-AN	AAAAANAAAA	GN	58	
LpMDHk2	:		GNGCCG	CCACCGA	ANAAAAAN	AAAAAN	28	
LpMDHk3	:	-----	GNGCCG	CAAGCA	AAAAAA	AAAAAG	27	
LpMDHk4	:	-----	GNGCCG	CANGGA	AAAAAN	AAAAAN	27	
LpMDHk5	:	-----	GCCCCG	CANNCAC	AAAAAN	AAAAAN	27	
LpMDHk6	:	-----	GCCG	CAACG	AAAAAA	AAAAAG	25	
LpMDHk7	:	-----	GTTTC	CAGAN	AAAAAC	GNAAANT	24	
LpMDHk8	:	-----	GTTTC	CAGAN	AAAAAC	GNAAANT	24	
LpMDHk9	:	-----	GNNAC	ACANAN	AAAAAC	AAAAAN	25	
LpMDHk10	:	-----	GTTAC	ACANAN	AAAAAC	AAAAAN	25	
LpMDHk11	:	-----	CCTCA	ACC	ANAAAA	AAAAAG	22	
LpMDHk12	:	-----	TTTCCC	ANAN	AGNAAAA	NTTAN	24	
LpMDHk13	:	-----	TTTCCC	AAAA	GNAAAA	NTTAN	23	
LpMDHk14	:	-----		ACACAN	ANAAAA	AAAAAN	22	
LpMDHk15	:	-----		ACACAN	ANAAAA	AAAAAN	22	
LpMDHk16	:	-----		ACACAN	AN	AA	AAAGAAAAAG	20
LpMDHk17	:	-----		CANNNNA	AA	AAAGAAAAAG	19	
LpMDHk18	:	-----		TTTCAA	AAAAAN	AAAAAG	21	
LpMDHk19	:	-----		GNACG	AAAAAA	AAAAAG	20	
LpMDHk20	:	-----		GNACG	AAAAAA	AAAAAG	20	
LpMDHk21	:	-----		GNACG	AAAAAA	AAAAAG	20	
LpMDHk22	:	-----		GNACG	AAAAAA	AAAAAG	20	
LpMDHk23	:	-----		CANAN	AAAAAN	AAAAAN	19	
LpMDHk24	:	-----		CANAN	AAAAAN	AAAAAN	19	
LpMDHk25	:	-----		CANAN	AAAAAC	AAAAAN	19	
LpMDHk26	:	-----		CANAN	AAAAAC	AAAAAN	19	
LpMDHk27	:	-----		CACCA	AAAAAA	AAAAAG	19	
LpMDHk28	:	-----		GACCA	AAAAAA	AAAAAG	19	
LpMDHk29	:	-----		ANNA	AAA	AAAAAG	19	
LpMDHk30	:	-----		ANAN	AAAAAN	AAAAAN	19	
LpMDHk31	:	-----		ANAN	AAAAAN	AAAAAN	19	
LpMDHk32	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk33	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk34	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk35	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk36	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk37	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk38	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk39	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk40	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk41	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk42	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk43	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk44	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk45	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk46	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk47	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk48	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk49	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk50	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk51	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk52	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk53	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk54	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk55	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk56	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk57	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk58	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk59	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk60	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk61	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk62	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk63	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk64	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk65	:	-----		NNAAAA	ANAAAA	AN	19	
LpMDHk66	:	-----		NNAAAA	ANAAAA	AN	19	

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LpMDHk1 : AGCCAGNACGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 118
LpMDHk2 : A-CCAGNA-GC-AGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 85
LpMDHk3 : AGCCAGNCGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 86
LpMDHk4 : A-CCAGNA-GC-AGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 84
LpMDHk5 : ANCCAGNA-GC-AGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 85
LpMDHk6 : AGCCAGNCGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 84
LpMDHk7 : ATCCAGNA-GC-AGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 82
LpMDHk8 : NNCCAGNACGC-AGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 83
LpMDHk9 : A-CCAGNA-GCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 83
LpMDHk10 : A-CCAGNA-GC-AGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 82
LpMDHk11 : AGCCAGNCGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 81
LpMDHk12 : NACCAGNN-GC-AGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 82
LpMDHk13 : NACCAGNA-GC-AGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 81
LpMDHk14 : ACCAGNAC-GC-AGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 80
LpMDHk15 : A-CCAGNA-GC-AGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 79
LpMDHk16 : NACCAGNA-GC-CAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 79
LpMDHk17 : NNCCAGNN-GC-CAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 78
LpMDHk18 : AGCCAG-NCGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 80
LpMDHk19 : AGCCAGNACGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 80
LpMDHk20 : AGCCAGNCGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 80
LpMDHk21 : AGCCAGNCGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 80
LpMDHk22 : AGCCAGNCGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 80
LpMDHk23 : ACCAGNN-GC-AGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 77
LpMDHk24 : ACCAGNN-GC-AGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 77
LpMDHk25 : A-CCAGNA-GCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 77
LpMDHk26 : ANCCAGNACGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 79
LpMDHk27 : AGCCAG-NCGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 78
LpMDHk28 : AGCCAGNCGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 79
LpMDHk29 : NCC-GNCC-CAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 74
LpMDHk30 : ANCCAGNACGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 78
LpMDHk31 : A-CCAGNACGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 76
LpMDHk32 : ANCCAGNA-GCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 75
LpMDHk33 : A-CCAGNACGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 75
LpMDHk34 : AGCCAGAG-GCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 75
LpMDHk35 : AGCCAG-ACGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 74
LpMDHk36 : A-CCAGNACGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 74
LpMDHk37 : A---A-GAAAAAANGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 67
LpMDHk38 : AAAAN-GAAAAAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 70
LpMDHk39 : ACCAGNAGGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 72
LpMDHk40 : AAAAA-GAAAAAANGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 69
LpMDHk41 : AAAAAAANAANAANGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 70
LpMDHk42 : A---N-GAAAAAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 66
LpMDHk43 : ACCAG-NNGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 70
LpMDHk44 : NACCAGNACGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 71
LpMDHk45 : A-CCAGNACGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 70
LpMDHk46 : AAAAA-NANAAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 68
LpMDHk47 : NACCAGNACGCAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 70
LpMDHk48 : AAAAA-NAAAAANGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 66
LpMDHk49 : AAAAA-GAAAAAANGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 65
LpMDHk50 : AAAAAAGAAAAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 67
LpMDHk51 : AAAAAAGAAAAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 66
LpMDHk52 : AAAAAANAAAAANGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 65
LpMDHk53 : AAAAAAGAAAAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 66
LpMDHk54 : AAAAAANAAAAANGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 64
LpMDHk55 : AAAAAAGAAAAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 63
LpMDHk56 : ---AAA-AAAAAANGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 57
LpMDHk57 : ---NANNAAAAAANGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 57
LpMDHk58 : -----CAAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 50
LpMDHk59 : -----ANAGGGGCGAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 43
LpMDHk60 : -----GAGCCGGGGCGCAGCAGCAATTCCCATCTGCTCAGCAACCC : 42
LpMDHk61 : -----GGGGGCGCAGCA-CAATTCCCATCTGCTCAGCAACCC : 37
LpMDHk62 : -----NCA-GCAGCAATTCCCATCTGCTCAGCAACCC : 31
LpMDHk63 : -----GNCACNCAATTCCCGNCTGCTCAGCAACCC : 31
LpMDHk64 : -----TCTGCTCAGCAACCC : 15
LpMDHk65 : ----- : -
LpMDHk66 : ----- : -

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[illegible]

240

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[illegible]

[illegible]

[illegible]

[illegible]



	*	740	*	760	*	780		
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LpMDHk2	:	-----					:	-
LpMDHk3	:	TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG					:	746
LpMDHk4	:	TNCACCTGT-----					:	692
LpMDHk5	:	TNCACCTGTGA-----					:	695
LpMDHk6	:	-----					:	-
LpMDHk7	:	-----					:	-
LpMDHk8	:	-----					:	-
LpMDHk9	:	TNCACCTGTGCCGATTGCTGCTGA-----					:	-
LpMDHk10	:	TCCACTGTGCCGATTGCTGCTGA-----					:	706
LpMDHk11	:	TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTNTACAACCCCAAGAAG					:	706
LpMDHk12	:	TNCACCTGTG-----					:	741
LpMDHk13	:	TNCACCTGTGCCGATTGCTGCTGAG-----					:	691
LpMDHk14	:	-----					:	705
LpMDHk15	:	TCCACTGTGCCGATTGCTGCTGAGAT-----					:	-
LpMDHk16	:	TNCACCTGTGCCGATTGCTGCTGAGATA-----					:	705
LpMDHk17	:	-----					:	706
LpMDHk18	:	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG					:	-
LpMDHk19	:	TCCACTGTGCCGATTGCTGCTGANATTCTGAAACAGAAAGGGCGNTTACAACCCCAAGNAAG					:	740
LpMDHk20	:	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG					:	740
LpMDHk21	:	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG					:	740
LpMDHk22	:	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG					:	740
LpMDHk23	:	-----					:	740
LpMDHk24	:	-----					:	-
LpMDHk25	:	TCCACTGTGCCGATTGCTGCT-----					:	-
LpMDHk26	:	TNCACCTGTGCCGATTGCTGCTGAGATTCTGAAAN-----					:	698
LpMDHk27	:	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG					:	713
LpMDHk28	:	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG					:	738
LpMDHk29	:	TNCACCTGTGC-----					:	739
LpMDHk30	:	TNCACCTGTGCCGATTGCT-----					:	684
LpMDHk31	:	TNCACCTGTGCCGATTGCTG-----					:	695
LpMDHk32	:	-----					:	695
LpMDHk33	:	-----					:	-
LpMDHk34	:	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAAGGGCGTNT-CCACCCCAAGAAG					:	-
LpMDHk35	:	TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG					:	734
LpMDHk36	:	TNCACCTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG					:	734
LpMDHk37	:	TCCACGGTGCCGATTGCTGNAAT-----					:	706
LpMDHk38	:	TCCACGGTGCCGATTGNTGCAAGAGATTCTGAAACAGAA-GGCGT-----					:	682
LpMDHk39	:	-----					:	712
LpMDHk40	:	TNCACGGTGCCGAT-----					:	-
LpMDHk41	:	TCCACGGTGCCGATTGCTGCAAGAGA-----					:	683
LpMDHk42	:	TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG					:	695
LpMDHk43	:	-----					:	726
LpMDHk44	:	TNCACCTGTGCCGATT-----					:	-
LpMDHk45	:	TNCACCTGTGCCGATTGCTGCTG-----					:	686
LpMDHk46	:	-----					:	693
LpMDHk47	:	-----					:	-
LpMDHk48	:	-----					:	-
LpMDHk49	:	TCCACGGTGCCGATTG-----					:	-
LpMDHk50	:	TCCACGGTGCCGATTGCTGCAAGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG					:	681
LpMDHk51	:	-----					:	727
LpMDHk52	:	TNCACGGTGCCGATN-----					:	-
LpMDHk53	:	TCCACGGTGCCGATTGCTGCAAGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG					:	680
LpMDHk54	:	TCCACGGTGCCGATTGCTGCAAGAGATTCTGAAACAGAG-----					:	726
LpMDHk55	:	TCCACGGTGCCGATTGCTGCAAGAGATTCTGAAACAGAAAGGGCGTCTACAACCCCAAGAAG					:	702
LpMDHk56	:	TNCACGGTGCCGATTGCTGCAAGAGATTCTGAAACA-AAAGGGCGTCTACAAC-----					:	723
LpMDHk57	:	TCCACGGTGCCGATTGNTGCA-ANATTITG-----					:	707
LpMDHk58	:	-----					:	687
LpMDHk59	:	TNC-----					:	-
LpMDHk60	:	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG					:	642
LpMDHk61	:	TNCACCTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG					:	702
LpMDHk62	:	-----					:	695
LpMDHk63	:	T-----					:	-
LpMDHk64	:	TNCACGGTGCCGATTGCTGCAAGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAA-----					:	630
LpMDHk65	:	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGGTCTACAACCCCAAGAAG					:	671
LpMDHk66	:	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGGTCTACAACCCCAAGAAG					:	407
	:						:	294



	*	800	*	820	*	840		
LpMDHk1	:	-----					:	-
LpMDHk2	:	-----					:	-
LpMDHk3	:	CTCTTCGGGGGTTTTCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCANA					:	801
LpMDHk4	:	-----					:	-
LpMDHk5	:	-----					:	-
LpMDHk6	:	-----					:	-
LpMDHk7	:	-----					:	-
LpMDHk8	:	-----					:	-
LpMDHk9	:	-----					:	-
LpMDHk10	:	-----					:	-
LpMDHk11	:	CTCTTCGGGGGTTTTCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCANAANAAN					:	801
LpMDHk12	:	-----					:	-
LpMDHk13	:	-----					:	-
LpMDHk14	:	-----					:	-
LpMDHk15	:	-----					:	-
LpMDHk16	:	-----					:	-
LpMDHk17	:	-----					:	-
LpMDHk18	:	CTCTTCGGGGGTTTCCACC					:	-
LpMDHk19	:	CTCTTCGGGGGTTTTCACCCTG					:	758
LpMDHk20	:	CTCTTCGGGGGTTTTCACCCTGGATGTTGTCAG					:	761
LpMDHk21	:	CTCTTCGGGGGTTTTCACCCTGGATGTTGTCAG					:	772
LpMDHk22	:	CTCTTCGGGGGTTTTCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCANAAGAAG					:	772
LpMDHk23	:	CTCTTCGGGGGTTTTCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCANAAGAAG					:	800
LpMDHk24	:	-----					:	-
LpMDHk25	:	-----					:	-
LpMDHk26	:	-----					:	-
LpMDHk27	:	CTCTTCGGGGGTTTTCACCCTGGATGTTGTCAG					:	-
LpMDHk28	:	CTCTTCGGGGGTTTTCACCCTGGATGTTGTCAGAG					:	771
LpMDHk29	:	-----					:	773
LpMDHk30	:	-----					:	-
LpMDHk31	:	-----					:	-
LpMDHk32	:	-----					:	-
LpMDHk33	:	-----					:	-
LpMDHk34	:	CTCTTCGGGGGTTTTCACCCTGGATGTTGTCAG					:	-
LpMDHk35	:	CTCTTCGGGGGTTTTCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCT					:	764
LpMDHk36	:	-----					:	785
LpMDHk37	:	-----					:	-
LpMDHk38	:	-----					:	-
LpMDHk39	:	-----					:	-
LpMDHk40	:	-----					:	-
LpMDHk41	:	-----					:	-
LpMDHk42	:	CTCTTCGGGGGTTTTCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCANAANAAG					:	786
LpMDHk43	:	-----					:	-
LpMDHk44	:	-----					:	-
LpMDHk45	:	-----					:	-
LpMDHk46	:	-----					:	-
LpMDHk47	:	-----					:	-
LpMDHk48	:	-----					:	-
LpMDHk49	:	-----					:	-
LpMDHk50	:	CTCTTCGGGGGTTTC					:	-
LpMDHk51	:	-----					:	741
LpMDHk52	:	-----					:	-
LpMDHk53	:	CTCTTCGGGGGTTTTCACCCTGGATGTTGTCAGAGCTAACACATT					:	-
LpMDHk54	:	-----					:	770
LpMDHk55	:	CTCTTCGGGGGTTTTCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCANA					:	-
LpMDHk56	:	-----					:	777
LpMDHk57	:	-----					:	-
LpMDHk58	:	-----					:	-
LpMDHk59	:	-----					:	-
LpMDHk60	:	CTCTTCGGGGGTTTTCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAGAAGAAG					:	762
LpMDHk61	:	CTCTTC					:	701
LpMDHk62	:	-----					:	-
LpMDHk63	:	-----					:	-
LpMDHk64	:	-----					:	-
LpMDHk65	:	CTCTTCGGGGGTTTTCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAGAAGAAG					:	467
LpMDHk66	:	CTCTTCGGGGGTTTTCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAGAAGAAG					:	354



	*	860	*	880	*	900	
LpMDHk1	:	-----		-----		-----	:
LpMDHk2	:	-----		-----		-----	:
LpMDHk3	:	-----		-----		-----	:
LpMDHk4	:	-----		-----		-----	:
LpMDHk5	:	-----		-----		-----	:
LpMDHk6	:	-----		-----		-----	:
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LpMDHk8	:	-----		-----		-----	:
LpMDHk9	:	-----		-----		-----	:
LpMDHk10	:	-----		-----		-----	:
LpMDHk11	:	A-----		-----		-----	802
LpMDHk12	:	-----		-----		-----	:
LpMDHk13	:	-----		-----		-----	:
LpMDHk14	:	-----		-----		-----	:
LpMDHk15	:	-----		-----		-----	:
LpMDHk16	:	-----		-----		-----	:
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LpMDHk21	:	-----		-----		-----	:
LpMDHk22	:	AACCTCA-----		-----		-----	807
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LpMDHk24	:	-----		-----		-----	:
LpMDHk25	:	-----		-----		-----	:
LpMDHk26	:	-----		-----		-----	:
LpMDHk27	:	-----		-----		-----	:
LpMDHk28	:	-----		-----		-----	:
LpMDHk29	:	-----		-----		-----	:
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LpMDHk35	:	-----		-----		-----	:
LpMDHk36	:	-----		-----		-----	:
LpMDHk37	:	-----		-----		-----	:
LpMDHk38	:	-----		-----		-----	:
LpMDHk39	:	-----		-----		-----	:
LpMDHk40	:	-----		-----		-----	:
LpMDHk41	:	-----		-----		-----	:
LpMDHk42	:	AACCTCAGCTTATCG-----		-----		-----	802
LpMDHk43	:	-----		-----		-----	:
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LpMDHk45	:	-----		-----		-----	:
LpMDHk46	:	-----		-----		-----	:
LpMDHk47	:	-----		-----		-----	:
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LpMDHk56	:	-----		-----		-----	:
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LpMDHk59	:	-----		-----		-----	:
LpMDHk60	:	AACCT-----		-----		-----	767
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LpMDHk62	:	-----		-----		-----	:
LpMDHk63	:	-----		-----		-----	:
LpMDHk64	:	-----		-----		-----	:
LpMDHk65	:	AACCTCAGCCTCATCGATGTTGATGTCCCAGTTGTCGGTGGCCATGCTGGGATCACGATT					527
LpMDHk66	:	AACCTCAGCCTCATCGATGTTGATGTCCCAGTTGTCGGTGGCCATGCTGGGATCACGATT					414



	*	920	*	940	*	960	
LpMDHk1	:	-----		-----		-----	:
LpMDHk2	:	-----		-----		-----	:
LpMDHk3	:	-----		-----		-----	:
LpMDHk4	:	-----		-----		-----	:
LpMDHk5	:	-----		-----		-----	:
LpMDHk6	:	-----		-----		-----	:
LpMDHk7	:	-----		-----		-----	:
LpMDHk8	:	-----		-----		-----	:
LpMDHk9	:	-----		-----		-----	:
LpMDHk10	:	-----		-----		-----	:
LpMDHk11	:	-----		-----		-----	:
LpMDHk12	:	-----		-----		-----	:
LpMDHk13	:	-----		-----		-----	:
LpMDHk14	:	-----		-----		-----	:
LpMDHk15	:	-----		-----		-----	:
LpMDHk16	:	-----		-----		-----	:
LpMDHk17	:	-----		-----		-----	:
LpMDHk18	:	-----		-----		-----	:
LpMDHk19	:	-----		-----		-----	:
LpMDHk20	:	-----		-----		-----	:
LpMDHk21	:	-----		-----		-----	:
LpMDHk22	:	-----		-----		-----	:
LpMDHk23	:	-----		-----		-----	:
LpMDHk24	:	-----		-----		-----	:
LpMDHk25	:	-----		-----		-----	:
LpMDHk26	:	-----		-----		-----	:
LpMDHk27	:	-----		-----		-----	:
LpMDHk28	:	-----		-----		-----	:
LpMDHk29	:	-----		-----		-----	:
LpMDHk30	:	-----		-----		-----	:
LpMDHk31	:	-----		-----		-----	:
LpMDHk32	:	-----		-----		-----	:
LpMDHk33	:	-----		-----		-----	:
LpMDHk34	:	-----		-----		-----	:
LpMDHk35	:	-----		-----		-----	:
LpMDHk36	:	-----		-----		-----	:
LpMDHk37	:	-----		-----		-----	:
LpMDHk38	:	-----		-----		-----	:
LpMDHk39	:	-----		-----		-----	:
LpMDHk40	:	-----		-----		-----	:
LpMDHk41	:	-----		-----		-----	:
LpMDHk42	:	-----		-----		-----	:
LpMDHk43	:	-----		-----		-----	:
LpMDHk44	:	-----		-----		-----	:
LpMDHk45	:	-----		-----		-----	:
LpMDHk46	:	-----		-----		-----	:
LpMDHk47	:	-----		-----		-----	:
LpMDHk48	:	-----		-----		-----	:
LpMDHk49	:	-----		-----		-----	:
LpMDHk50	:	-----		-----		-----	:
LpMDHk51	:	-----		-----		-----	:
LpMDHk52	:	-----		-----		-----	:
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LpMDHk54	:	-----		-----		-----	:
LpMDHk55	:	-----		-----		-----	:
LpMDHk56	:	-----		-----		-----	:
LpMDHk57	:	-----		-----		-----	:
LpMDHk58	:	-----		-----		-----	:
LpMDHk59	:	-----		-----		-----	:
LpMDHk60	:	-----		-----		-----	:
LpMDHk61	:	-----		-----		-----	:
LpMDHk62	:	-----		-----		-----	:
LpMDHk63	:	-----		-----		-----	:
LpMDHk64	:	-----		-----		-----	:
LpMDHk65	:	CTGCCTCTGTTGTCCAAGACTAGGCCTTCTGTCAGCTTCACGGACGAGGAAAC					587
LpMDHk66	:	CTGCCTCTGTTGTCCAAGACTAGGCCTTCTGTCAGCTTCACGGACGAGGAAAC					474

* 980 * 1000 * 1020

LpMDHk1	:	-----	:	-
LpMDHk2	:	-----	:	-
LpMDHk3	:	-----	:	-
LpMDHk4	:	-----	:	-
LpMDHk5	:	-----	:	-
LpMDHk6	:	-----	:	-
LpMDHk7	:	-----	:	-
LpMDHk8	:	-----	:	-
LpMDHk9	:	-----	:	-
LpMDHk10	:	-----	:	-
LpMDHk11	:	-----	:	-
LpMDHk12	:	-----	:	-
LpMDHk13	:	-----	:	-
LpMDHk14	:	-----	:	-
LpMDHk15	:	-----	:	-
LpMDHk16	:	-----	:	-
LpMDHk17	:	-----	:	-
LpMDHk18	:	-----	:	-
LpMDHk19	:	-----	:	-
LpMDHk20	:	-----	:	-
LpMDHk21	:	-----	:	-
LpMDHk22	:	-----	:	-
LpMDHk23	:	-----	:	-
LpMDHk24	:	-----	:	-
LpMDHk25	:	-----	:	-
LpMDHk26	:	-----	:	-
LpMDHk27	:	-----	:	-
LpMDHk28	:	-----	:	-
LpMDHk29	:	-----	:	-
LpMDHk30	:	-----	:	-
LpMDHk31	:	-----	:	-
LpMDHk32	:	-----	:	-
LpMDHk33	:	-----	:	-
LpMDHk34	:	-----	:	-
LpMDHk35	:	-----	:	-
LpMDHk36	:	-----	:	-
LpMDHk37	:	-----	:	-
LpMDHk38	:	-----	:	-
LpMDHk39	:	-----	:	-
LpMDHk40	:	-----	:	-
LpMDHk41	:	-----	:	-
LpMDHk42	:	-----	:	-
LpMDHk43	:	-----	:	-
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LpMDHk45	:	-----	:	-
LpMDHk46	:	-----	:	-
LpMDHk47	:	-----	:	-
LpMDHk48	:	-----	:	-
LpMDHk49	:	-----	:	-
LpMDHk50	:	-----	:	-
LpMDHk51	:	-----	:	-
LpMDHk52	:	-----	:	-
LpMDHk53	:	-----	:	-
LpMDHk54	:	-----	:	-
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LpMDHk56	:	-----	:	-
LpMDHk57	:	-----	:	-
LpMDHk58	:	-----	:	-
LpMDHk59	:	-----	:	-
LpMDHk60	:	-----	:	-
LpMDHk61	:	-----	:	-
LpMDHk62	:	-----	:	-
LpMDHk63	:	-----	:	-
LpMDHk64	:	-----	:	-
LpMDHk65	:	CTGACAAAGAGGATACAGAACGCTGGGACAGAGGCTGGTGGAGGCGAA-----	:	634
LpMDHk66	:	CTGACAAAGAGGATACAGAACGCTGGGACAGAGGCGGTGGAGGCCAAGGCTGGTGGCTGGC-----	:	534

	*	1040	*	1060	*	1080
LpMDHk1	:	-----		-----		-----
LpMDHk2	:	-----		-----		-----
LpMDHk3	:	-----		-----		-----
LpMDHk4	:	-----		-----		-----
LpMDHk5	:	-----		-----		-----
LpMDHk6	:	-----		-----		-----
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LpMDHk61	:	-----		-----		-----
LpMDHk62	:	-----		-----		-----
LpMDHk63	:	-----		-----		-----
LpMDHk64	:	-----		-----		-----
LpMDHk65	:	-----		-----		-----
LpMDHk66	:	TCTGCTACTCTGTCCATGGCTTATGCCGCTGCCAGATTGTTGAGTCATCGCTCCGCGCA				



	*	1100	*	1120	*	1140	
LpMDHk1	:	-----		-----		-----	:
LpMDHk2	:	-----		-----		-----	:
LpMDHk3	:	-----		-----		-----	:
LpMDHk4	:	-----		-----		-----	:
LpMDHk5	:	-----		-----		-----	:
LpMDHk6	:	-----		-----		-----	:
LpMDHk7	:	-----		-----		-----	:
LpMDHk8	:	-----		-----		-----	:
LpMDHk9	:	-----		-----		-----	:
LpMDHk10	:	-----		-----		-----	:
LpMDHk11	:	-----		-----		-----	:
LpMDHk12	:	-----		-----		-----	:
LpMDHk13	:	-----		-----		-----	:
LpMDHk14	:	-----		-----		-----	:
LpMDHk15	:	-----		-----		-----	:
LpMDHk16	:	-----		-----		-----	:
LpMDHk17	:	-----		-----		-----	:
LpMDHk18	:	-----		-----		-----	:
LpMDHk19	:	-----		-----		-----	:
LpMDHk20	:	-----		-----		-----	:
LpMDHk21	:	-----		-----		-----	:
LpMDHk22	:	-----		-----		-----	:
LpMDHk23	:	-----		-----		-----	:
LpMDHk24	:	-----		-----		-----	:
LpMDHk25	:	-----		-----		-----	:
LpMDHk26	:	-----		-----		-----	:
LpMDHk27	:	-----		-----		-----	:
LpMDHk28	:	-----		-----		-----	:
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LpMDHk30	:	-----		-----		-----	:
LpMDHk31	:	-----		-----		-----	:
LpMDHk32	:	-----		-----		-----	:
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LpMDHk38	:	-----		-----		-----	:
LpMDHk39	:	-----		-----		-----	:
LpMDHk40	:	-----		-----		-----	:
LpMDHk41	:	-----		-----		-----	:
LpMDHk42	:	-----		-----		-----	:
LpMDHk43	:	-----		-----		-----	:
LpMDHk44	:	-----		-----		-----	:
LpMDHk45	:	-----		-----		-----	:
LpMDHk46	:	-----		-----		-----	:
LpMDHk47	:	-----		-----		-----	:
LpMDHk48	:	-----		-----		-----	:
LpMDHk49	:	-----		-----		-----	:
LpMDHk50	:	-----		-----		-----	:
LpMDHk51	:	-----		-----		-----	:
LpMDHk52	:	-----		-----		-----	:
LpMDHk53	:	-----		-----		-----	:
LpMDHk54	:	-----		-----		-----	:
LpMDHk55	:	-----		-----		-----	:
LpMDHk56	:	-----		-----		-----	:
LpMDHk57	:	-----		-----		-----	:
LpMDHk58	:	-----		-----		-----	:
LpMDHk59	:	-----		-----		-----	:
LpMDHk60	:	-----		-----		-----	:
LpMDHk61	:	-----		-----		-----	:
LpMDHk62	:	-----		-----		-----	:
LpMDHk63	:	-----		-----		-----	:
LpMDHk64	:	-----		-----		-----	:
LpMDHk65	:	-----		-----		-----	:
LpMDHk66	:	ATGGCTGGTGATCCAGATGTTTACGAGTGCACGTATGTTTCAGTCTGAGTTAACAGAGCTT					:

	* 1160 *	1180 *	1200
LpMDHk1	:	-----	:
LpMDHk2	:	-----	:
LpMDHk3	:	-----	:
LpMDHk4	:	-----	:
LpMDHk5	:	-----	:
LpMDHk6	:	-----	:
LpMDHk7	:	-----	:
LpMDHk8	:	-----	:
LpMDHk9	:	-----	:
LpMDHk10	:	-----	:
LpMDHk11	:	-----	:
LpMDHk12	:	-----	:
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LpMDHk14	:	-----	:
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LpMDHk19	:	-----	:
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LpMDHk41	:	-----	:
LpMDHk42	:	-----	:
LpMDHk43	:	-----	:
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LpMDHk45	:	-----	:
LpMDHk46	:	-----	:
LpMDHk47	:	-----	:
LpMDHk48	:	-----	:
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LpMDHk58	:	-----	:
LpMDHk59	:	-----	:
LpMDHk60	:	-----	:
LpMDHk61	:	-----	:
LpMDHk62	:	-----	:
LpMDHk63	:	-----	:
LpMDHk64	:	-----	:
LpMDHk65	:	-----	:
LpMDHk66	:	CCATTCTTCGCGTCCAGAGTTAAGCTTGGGAAGGACGGNGTTGAGTCCATCATTTCTCTCC	:



	* 1220	* 1240	* 1260
LpMDHk1	:	-----	-----
LpMDHk2	:	-----	-----
LpMDHk3	:	-----	-----
LpMDHk4	:	-----	-----
LpMDHk5	:	-----	-----
LpMDHk6	:	-----	-----
LpMDHk7	:	-----	-----
LpMDHk8	:	-----	-----
LpMDHk9	:	-----	-----
LpMDHk10	:	-----	-----
LpMDHk11	:	-----	-----
LpMDHk12	:	-----	-----
LpMDHk13	:	-----	-----
LpMDHk14	:	-----	-----
LpMDHk15	:	-----	-----
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LpMDHk60	:	-----	-----
LpMDHk61	:	-----	-----
LpMDHk62	:	-----	-----
LpMDHk63	:	-----	-----
LpMDHk64	:	-----	-----
LpMDHk65	:	-----	-----
LpMDHk66	:	GACCTGGAGGGAGTGACGGAGTACGAGGCCAAGGCGCTTGANGCATTGAAGGCTGAGCTG	774

LpMDHk1 : --- : -
LpMDHk2 : --- : -
LpMDHk3 : --- : -
LpMDHk4 : --- : -
LpMDHk5 : --- : -
LpMDHk6 : --- : -
LpMDHk7 : --- : -
LpMDHk8 : --- : -
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LpMDHk60 : --- : -
LpMDHk61 : --- : -
LpMDHk62 : --- : -
LpMDHk63 : --- : -
LpMDHk64 : --- : -
LpMDHk65 : --- : -
LpMDHk66 : AAG : 777

Figure 38 Nucleotide sequence of LpMDH1

LpMDH1 : GNAACAGNNGCGNCTTTTCCTNCANTGTTGCCGTGCAATCGCTGANAAGTATCCAGAAA : 60

LpMDH1 : TCATATACGAGGAAGTAATTATTGATAACTGCTGTATGACGCTCGTGAAGAACCCTGGTA : 120

LpMDH1 : CGTTTGATGTATTAGTGATGCCAAATCTATATGGCGACATTATTAGTGATCTATGTGCTG : 180

LpMDH1 : GTTTGATCGGAGGCTTGGGCCTAACTCCCAGCTGCAACATTGGTGAAGGTGGCATTGTGTC : 240

LpMDH1 : TTGCAGAGGCTGTCCATGGCTCTGCACCTGATATATCTGGCAAGAACCTGGCAAACCCAA : 300

LpMDH1 : CTGCTCTTATGCTGAGTGCTGTTATGATGTTGCGCCACTTGCAATTNAACGACCAAGCAN : 360

LpMDH1 : AACGGATCCACAATGCTATCCTCCAGACTATCGNCGAGGGGAAGNACANAAGT : 414

Figure 39 Deduced amino acid sequence of LpMDH1

LpMDH1 : KQXXLFXXCCRAIAXKYPEIIYEVIIDNCCMTLVKNPGTFDVLVMPNLYGDIISDLCAG : 60

LpMDH1 : LIGGLGLTPSCNIGEGGICLAEAVHGSAPDISGKNLANPTALMLSAVMMLRHLQXNDQAX : 120

LpMDH1 : RIHNAILQTIXEGKXXT : 137

Figure 40 Nucleotide sequence of LpMDHm

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      *      20      *      40      *      60
LpMDHm : GNCACCNCCAGNNACAACTCTGGTACCTCAATTGCTACTCCACACCTCACTACTTCTACC : 60

      *      80      *      100     *      120
LpMDHm : AATCCACTACACAGCTTCGAGCTACCCCGCCCCCGCAATCCAAACTACCTCTCCCTAGCA : 120

      *      140     *      160     *      180
LpMDHm : AATCTACAACATGAAGGCAGTCGTAGCTGGAGCCGCCGGTGGCATTGGACAGCCATTGTC : 180

      *      200     *      220     *      240
LpMDHm : CCTCCTCCTTAAGACCTGCCCCGCTCGTCACTGAGCTCGCCCTATACGATGTCGTCAACGC : 240

      *      260     *      280     *      300
LpMDHm : CGTCGGTGTCGCGACTGACCTCTCCACATCTCCTCGCCCCGAAAGTAACCGGCTACCT : 300

      *      320     *      340     *      360
LpMDHm : GCCGGCAAATGACGGTATGCAGCAGGCTCTCACTGGCGCCGACATCGTGGTCATCCCCGC : 360

      *      380     *      400     *      420
LpMDHm : TGGTATTCCCCGCAAGCCCGGCATGACCCGTGACGACCTCTTCAAGATCAACGCCGGCAT : 420

      *      440     *      460     *      480
LpMDHm : TGTCCAGGGTCTCATCGAGGGTGTCGCCAAGCACTGCCCCAAGGCATACGTTCTCGTCAT : 480

      *      500     *      520     *      540
LpMDHm : CTCCAACCCCGTCAACTCGACTGTGCCCATCGCCGCCGAGGTGCTGAAGAAGGCCGGTGT : 540

      *      560     *      580     *      600
LpMDHm : CTTGACCCCAAGAAGCTCTTCGGTGTCAACACCCTCGATGTCGTCCGCGCCGAGACCTT : 600

      *      620     *      640     *
LpMDHm : CGTTGCCGAGATCACTGGCGAGAAGGACCCAGCGAAGTTGAACATNCCCGTA : 652

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Figure 41 . Deduced amino acid sequence of LpMDHm

LpMDHm : * 20 * 40 * 60
: XXPXTTLVPQLLLHTSLLLPIHYTASSYPAPAIQTTSP*QIYNMKAVVAGAAGGIGQPLS : 59

LpMDHm : * 80 * 100 * 120
: LLLKTCPLVTELALYDVVNAVGVATDLSHISSPAKVTGYLPANDGMQQALTGADIVVIPA : 119

LpMDHm : * 140 * 160 * 180
: GIPRKPGMTRDDLFFKINAGIVQGLIEGVAKHCPKAYVLVISNPVNSTVPAAEVLKKAGV : 179

LpMDHm : * 200 *
: FDPKKLFGVTTLDVVRAETFVAEITGEKDPKLNXPV : 216

Figure 42 Nucleotide sequence of LpPEPCa

LpPEPCa : GNGTACACGAAATAGAAATCAACGGAAAGCANGAAGTGATGATTGGGTATCAGCATTCTGG : 60

LpPEPCa : GAAGGATGCTGGCCGTTTCTCTGCTGGTTGGCACTTGTACAAAGCTCAAGAGGAGCTTAT : 120

LpPEPCa : TAAGGTTGCGGAGACGTTTGGGGTTAAGNTGACTATGTTTCATGGACGAGGGGGTACTGT : 180

LpPEPCa : TGGAAGAGGTGGCGGCCCTACCCATCTTGCTATACTGTCACAACCTCCAGATACTGTCCA : 240

LpPEPCa : TGGATCACTTCGGGTAAGTGTCAAGGTGAAGTCATTGAGCAGTCCTTCGGAGAGGAGCA : 300

LpPEPCa : TTTGTGTTTTAGAACGCTTCAACGTTTTACAGCTGCTACTCTTGAACATGGTATGCATCC : 360

LpPEPCa : ACCAATCTCACCTAAACCAGAAATGGCGTGCTTTGATGGATGAAATGGCTGTTGTTGCCAC : 420

LpPEPCa : AGAGGAATACCGTTCCATTGTTTTCCAAGAACCAAGATTTGTTGAGTATTTCCGCCTTGC : 480

LpPEPCa : AACACCAGAGCTCGAGTATGGTAGGATGAATATTGGAAGCAGGCCATCAAAACGTAAGCC : 540

LpPEPCa : AAGCGGAGGAATCGAATCATTGCGTGCAATTCCTTGATATTTGCTTGGACACAGACTAG : 600

LpPEPCa : ATTCCACCTGCCAGTGTGGCTTGNTTTGGTGCGGCCTTCAAGCATGTCCTGCAAAAGGA : 660

LpPEPCa : CATTGCGTANTCTTCAAATCCTTCAGCAGATGTACAACGAGTGGCCGTTTAGGGTTACCAT : 720

LpPEPCa : AAACCTGGTTGAGATGGTGTGTTGCCAAGGGCGATCCAGGTATAGCAGCT : 769

Figure 43 Deduced amino acid sequence of LpPEPca

* 20 * 40 * 60
LpPEPCa : XTRNRINGKXEVMIGYQHSGKDAGRFSAGWHLYKAQEELIKVAETFGVKXTMFHGRGGTV : 60

* 80 * 100 * 120
LpPEPCa : GRGGGPTHLAISQPPDTVHGSRLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHP : 120

* 140 * 160 * 180
LpPEPCa : PISPKPEWRALMDEMAVVATEEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSRPSKRKP : 180

* 200 * 220 * 240
LpPEPCa : SGGIESLRAIPWIFAWTQTRFHLPVWLXFGAAFKHVLQKDIRXLQILQOMYNEWPFRTI : 240

*
LpPEPCa : NLVEMVFAKGDPGIAA : 256

Figure 44 Consensus contig nucleotide sequence of LpPEPCb

```

      *           20           *           40           *           60
LpPEPCb : GAAGAAGTTGCTGATGTTTTAAGNACATTTNTGTCCTTGACAGAGCTCCCAGCAGATTGTT : 60

      *           80           *           100          *           120
LpPEPCb : TTGGTGCTTACATCATCTCAATGGCAACTGCCCCATCTGATGTGCTTGCTGTTGAGCTTT : 120

      *           140          *           160          *           180
LpPEPCb : TGCAGCGGGAGTGCCATATAAAAAAGCCATTGAGAGTTGTTCCACTATTTGAAAAGCTTG : 180

      *           200          *           220          *           240
LpPEPCb : CAGATCTTGAANCAGCTCCAGCATCTGTTGCACGACTATTTTCAATAGACTGGTACATGA : 240

      *           260          *           280          *           300
LpPEPCb : ATAGAATCAATGGCAAGCAGGAGGTCATGATTGGATACTCAGACTCTGGGAAGGACGCTG : 300

      *           320          *           340          *           360
LpPEPCb : GCGTCTCTCTGCAGCGTGGCAAATGTATAAAGCACAGAAGATCTCATAAAGGTGGCAA : 360

      *           380          *           400          *           420
LpPEPCb : AGCAATATGGAGTAAAGTTAACAATGTTTCATGGAAGAGGTGGAACGGTTGGCAGAGGAG : 420

      *           440          *           460          *           480
LpPEPCb : GTGGTCCCAGTCATCTTGCTATATTATCTCAACCACCAGACAGATAACAAGGATCACTTC : 480

      *           500          *           520          *           540
LpPEPCb : GTGTAACAGTTCAAGGCGAGGTCATAGAGCACTCATTTGGAGAGGAACACTTGTGCTTCA : 540

      *           560          *           580          *           600
LpPEPCb : GAACTCTGCAACGTTTCACCTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTAC : 600

      *           620          *           640          *           660
LpPEPCb : CCAAGCCAGAATGGCGTGCTATAATGGATGAGATGGCTGTAGTGGCAACAAAAGAATATC : 660

      *           680          *           700          *           720
LpPEPCb : GATCAATTGTCTTCCAAGAACCACGTTTTGTGCGAATACTTCCGCTCGGCAACACCTGAGA : 720

      *           740          *           760          *           780
LpPEPCb : CTGAATATGGTCGGATGAATATTGGTAGCCGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 780

      *           800          *           820          *           840
LpPEPCb : TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGACACAGACAAGGTTTCATCTTC : 840

      *           860          *           880          *           900
LpPEPCb : CTGTATGGCTTGGATTGTTGTCAGCGTTCAAACATATCATGCAGAAGGACATCAGGAATA : 900

      *           920          *           940          *           960
LpPEPCb : TCCATACTCTGAAAGAAATGTACAATGAGTGGCCATTCTTTAGGGTCACCCTTGACTTGC : 960

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* 980 * 1000 * 1020
 LpPEPCb : TTGAGATGGTTTGTGCCAAGGGAGATCCAGGAATTGCTGCTTTATATGACAAATTGCTTG : 1020

* 1040 * 1060 * 1080
 LpPEPCb : TGTCTGAAGATCTGCAGCCCTTTGGGGAGCAGCTGAGAAACAACTTTGAAGAGACGAAAC : 1080

* 1100 * 1120 * 1140
 LpPEPCb : AGTTACTCCTTCAGGTTGCTGGCCACAAGGACGTTCTTGAAGGGGATCCTTACCTGAAGC : 1140

* 1160 * 1180 * 1200
 LpPEPCb : AGCGTCTGCGGTTGCGTGAGTCATACATCACAAACATTGAATGTTTGCCAAGCCNACACCC : 1200

* 1220 * 1240 * 1260
 LpPEPCb : TGAAGCGGATAAGAGACCCTAGCTTCGAGGTGACACCGCAGCAGGCACCTCTGTGGAAGG : 1260

* 1280 * 1300 * 1320
 LpPEPCb : AGTTCGCTGATGAGAAGGAGCCAGCTGAGCTGGTGCAACTGAACCGTGGGAGCGAGTACG : 1320

* 1340 * 1360 * 1380
 LpPEPCb : CCCCAGGCCTGGAGGACACCCTCATCCTTACCATGAAGGGTATTTGCTGTGGAATGCAAA : 1380

* 1400 * 1420 * 1440
 LpPEPCb : ACACAGGCTAGGCCAGTTTGCCTATTTGGAATAACTGTCATCCCGTCAGATGGGGCGTGA : 1440

* 1460 * 1480 * 1500
 LpPEPCb : ATATGTGTGTTCCCCAAATGCTAGTGAACCCTGGAGGCATTTTGGCCACTTACATGCCTT : 1500

* 1520 * 1540 * 1560
 LpPEPCb : TTGGTTATGGATGNACTTTGATCTTAATGNCAAGGGTTGTTGAAGCCTGATCTAAATAAA : 1560

* 1580 * 1600 * 1620
 LpPEPCb : ATATGGAACAATGATATTCTGGTNGGATCTAATAATTTGCTTGGCTCTGGCATCGNAATA : 1620

* 1640
 LpPEPCb : GNGATTTGGAGTNGTTTAAC : 1640

Figure 45 Deduced amino acid sequence of LpPEPCb

LpPEPCb : RSCXCFKXIXVLAELPADCFGAYIISMATAPSDVLAVELLQRECHIKPLRVVPLFEKLA : 60

LpPEPCb : DLEXAPASVARLFSIDWYMNRINGKQEVMI GYSDSGKDAGRLSAAWQMYKAQEDLIKVAK : 120

LpPEPCb : QYGVKLTMFHGRGGTVGRGGGPSHLAILSQPPDTIQGSLRVTVQGEVIEHSFGEEHLCFR : 180

LpPEPCb : TLQRF TAATLEHGMHPPISP KPEWRAIMDEMAVVATKEYRSIVFQEPRFVEYFRSATPET : 240

LpPEPCb : EYGRMNIGSRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGA AFKHIMQKDIRNI : 300

LpPEPCb : HTLKEMYNEWPF FRVTLDLLEMVF AKGDPGIAALYDKLLVSEDLPQPFGEQLRNNFEETKQ : 360

LpPEPCb : LLLQVAGHKDVL EGD P YLKQRLRLRESYITTLNVCQAXTLKRIRDPSFEVTPQQAPLSKE : 420

LpPEPCb : FADEKEPAELVQLNRGSEYAPGLEDTLILTMKGICCGMQNTG : 462

Figure 46 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpPEPCb

		*	20	*	40	*	60	
LpPEPCb1 :	GAAGAAGTTGCTGATGTTTTAAGNACATTTNTGTCCTTGCAGAGCTCC	CAGCAGATTGTT	:	60				
LpPEPCb2 :	-----	-----	:	-				
LpPEPCb3 :	-----	-----	:	-				
LpPEPCb4 :	-----	-----	:	-				
LpPEPCb5 :	-----	-----	:	-				
LpPEPCb6 :	-----	-----	:	-				
		*	80	*	100	*	120	
LpPEPCb1 :	TTGGTGCTTACATCATCTCAATGGCAACTGCCCCATCTGATGTGCTT	CTGTTGAGCTTT	:	120				
LpPEPCb2 :	-----	-----	:	-				
LpPEPCb3 :	-----	-----	:	-				
LpPEPCb4 :	-----	-----	:	-				
LpPEPCb5 :	-----	-----	:	-				
LpPEPCb6 :	-----	-----	:	-				
		*	140	*	160	*	180	
LpPEPCb1 :	TGCAGCGGGAGTGCCATATAAAAAAGCCATTGAGAGTTGTTCCACTA	TTTGAAAAGCTTG	:	180				
LpPEPCb2 :	-----	-----	:	-				
LpPEPCb3 :	-----	-----	:	-				
LpPEPCb4 :	-----	-----	:	-				
LpPEPCb5 :	-----	-----	:	-				
LpPEPCb6 :	-----	-----	:	-				
		*	200	*	220	*	240	
LpPEPCb1 :	CAGATCTTGAANCAGCTCCAGCATCTGTTGCACGACTATTTTCAATAGACTGGTACATGA	:	240					
LpPEPCb2 :	-----	-----	:	-				
LpPEPCb3 :	-----	-----	:	-				
LpPEPCb4 :	-----	-----	:	-				
LpPEPCb5 :	-----	-----	:	-				
LpPEPCb6 :	-----	-----	:	-				
		*	260	*	280	*	300	
LpPEPCb1 :	ATAGAATCAATGGCAAGCAGGAGGTGATGATTGGATACTCAGACTCT	GGGAAGGACGCTG	:	300				
LpPEPCb2 :	-----	-----	:	-				
LpPEPCb3 :	-----	-----	:	-				
LpPEPCb4 :	-----	-----	:	-				
LpPEPCb5 :	-----	-----	:	-				
LpPEPCb6 :	-----	-----	:	-				
		*	320	*	340	*	360	
LpPEPCb1 :	GGCGTCTCTCTGCAGCGTGGCAAATGTATAAAGCACAAAGAAGATCTGATAAAGGTGGCAA	:	360					
LpPEPCb2 :	-----GTATAAAGCACAAAGAAGATCTGATAAAGGTGGCAA	:	35					
LpPEPCb3 :	-----	-----	:	-				
LpPEPCb4 :	-----	-----	:	-				
LpPEPCb5 :	-----	-----	:	-				
LpPEPCb6 :	-----	-----	:	-				
		*	380	*	400	*	420	
LpPEPCb1 :	AGCAATATGGAGTAAAGTTAACAATGTTTCATGGAAGAGGTGGAACGGTTGGCAGAGGAG	:	420					
LpPEPCb2 :	AGCAATATGGAGTAAAGTTAACAATGTTTCATGGAAGAGGTGGAACGGTTGGCAGAGGAG	:	95					
LpPEPCb3 :	-----AATGTTT-NTGGAAGAGGTGGAACGGTTGGCAGAGGAG	:	37					
LpPEPCb4 :	-----GCA ⁵ AGGAG	:	9					
LpPEPCb5 :	-----	-----	:	-				
LpPEPCb6 :	-----	-----	:	-				

	*	440	*	460	*	480	
LpPEPCb1 :	GTGGTCCCAGTCATCTTGCTATATTATCTCAACCACCAGACACGATAAAGGATCACTTC						: 480
LpPEPCb2 :	GTGGTCCCAGTCATCTTGCTATATTATCTCAACCACCAGACACGATAAAGGATCACTTC						: 155
LpPEPCb3 :	GTGGTCCCAGTCATCTTGCTATATTATCTCAACCACAGACACGATAAAGGATCACTTC						: 97
LpPEPCb4 :	GTGGTCCCAGTCATCTTGCTATATTATCTCAACCACCAGACACGATAAAGGATCACTTC						: 69
LpPEPCb5 :	-----						: -
LpPEPCb6 :	-----						: -

	*	500	*	520	*	540	
LpPEPCb1 :	GTGTAACAGTTCAAGGCGAGGTCATAGAGCACTCATTTGGAGAGGAACTTGTGCTTCA						: 540
LpPEPCb2 :	GTGTAACAGTTCAAGGCGAGGTCATAGAGCACTCATTTGGAGAGGAACTTGTGCTTCA						: 215
LpPEPCb3 :	GTGTAACAGTTCAAGGCGAGGTCATAGAGCACTCATTTGGAGAGGAACTTGTGCTTCA						: 157
LpPEPCb4 :	GTGTAACAGTTCAAGGCGAGGTCATAGAGCACTCATTTGGAGAGGAACTTGTGCTTCA						: 129
LpPEPCb5 :	-----						: -
LpPEPCb6 :	-----						: -

	*	560	*	580	*	600	
LpPEPCb1 :	GAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCC						: 600
LpPEPCb2 :	GAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCC						: 275
LpPEPCb3 :	GAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCC						: 217
LpPEPCb4 :	GAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCC						: 189
LpPEPCb5 :	-----						: -
LpPEPCb6 :	-----						: -

	*	620	*	640	*	660	
LpPEPCb1 :	CCAAACCCAGAATGGCCTTGCTATAATGGATGATATGGCTGTAGTGGCAACAAAAGAAATATC						: 660
LpPEPCb2 :	CCAAGCCAGAATGGCGTGCTATAATGGATGAGATGGCTGTAGTGGCAACAAAAGAAATATC						: 335
LpPEPCb3 :	CCAAGCCAGAATGGCGTGCTATAATGGATGAGATGGCTGTAGTGGCAACAAAAGAAATATC						: 277
LpPEPCb4 :	CCAAGCCAGAATGGCGTGCTATAATGGATGAGATGGCTGTAGTGGCAACAAAAGAAATATC						: 249
LpPEPCb5 :	-----						: -
LpPEPCb6 :	-----						: -

	*	680	*	700	*	720	
LpPEPCb1 :	GATCAATTGCTCTTCCAAGAACCACGTTTTGTGCGAATACTTCCGCTCGGCAACACCTGAGA						: 697
LpPEPCb2 :	GATCAATTGCTCTTCCAAGAACCACGTTTTGTGCGAATACTTCCGCTCGGCAACACCTGAGA						: 395
LpPEPCb3 :	GATCAATTGCTCTTCCAAGAACCACGTTTTGTGCGAATACTTCCGCTCGGCAACACCTGAGA						: 337
LpPEPCb4 :	GATCAATTGCTCTTCCAAGAACCACGTTTTGTGCGAATACTTCCGCTCGGCAACACCTGAGA						: 309
LpPEPCb5 :	-----						: -
LpPEPCb6 :	-----						: -

	*	740	*	760	*	780	
LpPEPCb1 :	-----						: -
LpPEPCb2 :	CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGAGGCA						: 455
LpPEPCb3 :	CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGAGGCA						: 397
LpPEPCb4 :	CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGAGGCA						: 369
LpPEPCb5 :	-----						: -
LpPEPCb6 :	-----						: -

	*	800	*	820	*	840	
LpPEPCb1 :	-----						: -
LpPEPCb2 :	TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC						: 515
LpPEPCb3 :	TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC						: 457
LpPEPCb4 :	TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC						: 429
LpPEPCb5 :	-----						: -
LpPEPCb6 :	-----						: -



	*	860	*	880	*	900	
LpPEPCb1 :	-----		-----		-----		-
LpPEPCb2 :		CTGTATGGCTTGGATTGGTGCAGCGTTCAAACATATCATGCAGAAGGACATCAGGAATA					: 575
LpPEPCb3 :		CTGTATGGCTTGGATTGGTGCAGCGTTCAAACATATCATGCAGAAGGACATCAGGAATA					: 517
LpPEPCb4 :		CTGTATGGCTTGGATTGGTGCAGCGTTCAAACATATCATGCAGAAGGACATCAGGAATA					: 489
LpPEPCb5 :	-----		-----		-----		-
LpPEPCb6 :	-----		-----		-----		-

	*	920	*	940	*	960	
LpPEPCb1 :	-----		-----		-----		-
LpPEPCb2 :		TCCATACTCTGAAAGAAATGTACAATGAGTGGCCATTCTTTAGGGTCACCCCTTGACTTGC					: 635
LpPEPCb3 :		TCCATACTCTGAAAGAAATGTACAATGAGTGGCCATTCTTTAGGGTCACCCCTTGACTTGC					: 577
LpPEPCb4 :		TCCATACTCTGAAAGAAATGTACAATGAGTGGCCATTCTTTAGGGTCACCCCTTGACTTGC					: 549
LpPEPCb5 :	-----		-----		-----		-
LpPEPCb6 :	-----		-----		-----		-

	*	980	*	1000	*	1020	
LpPEPCb1 :	-----		-----		-----		-
LpPEPCb2 :		TTGAGATGGTTTTTTGCCAAGGGAGATCCAGGAATTGCTGCTTTATATGACAAATTGCTTG					: 695
LpPEPCb3 :		TTGAGATGGTTTTTTGCCAAGGGAGATCCAGGAATTGCTGCTTTATATGACAAATTGCTTG					: 637
LpPEPCb4 :		TTGAGATGGTTTTTTGCCAAGGGAGATCCAGGAATTGCTGCTTTATATGACAAATTGCTTG					: 609
LpPEPCb5 :		-----GGTTTTG-CNAGGGAGATCC-GG-ATTGCTGCTTTATATGACAAATTGCTTG					: 50
LpPEPCb6 :	-----		-----		-----		-

	*	1040	*	1060	*	1080	
LpPEPCb1 :	-----		-----		-----		-
LpPEPCb2 :		TGTCTGAAGATCTGCAGCCCTTTGGGGAGCAGCTGAGAAACAACCTTTGAAGAGACGAAAC					: 755
LpPEPCb3 :		TGTCTGAAGATCTGCAGCCCTTTGGGGAGCAGCTGAGAAACAACCTTTGAAGAGACGAAAC					: 697
LpPEPCb4 :		TGTCTGAAGATCTGCAGCCCTTTGGGGAGCAGCTGAGAAACAACCTTTGAAGAGACGAAAC					: 669
LpPEPCb5 :		TGTCTGAAGATCTGCAGCCCTTTGGGGAGCAGCTGAGAAACAACCTTTGAAGAGACGAAAC					: 110
LpPEPCb6 :	-----		-----		-----		-

	*	1100	*	1120	*	1140	
LpPEPCb1 :	-----		-----		-----		-
LpPEPCb2 :		AGNTACTCTTTAAGGTTGCTGNCACCAAGG-----					: 785
LpPEPCb3 :		AGTTACTCCTTCAGGTTGCTGGCCACAAGGACGTTCTTGAAGGGGATCCTTACCTGAAGC					: 757
LpPEPCb4 :		AGTTACTCCTTCAGGTTGCTGGCCACAAGGACGTTCTTGAAGGGGATCCTTACCTGAAGC					: 729
LpPEPCb5 :		AGTTACTCCTTCAGGTTGCTGGCCACAAGGACGTTCTTGAAGGGGATCCTTACCTGAAGC					: 170
LpPEPCb6 :	-----		-----GGACGTTCTTGAAGGGGATCCTTACCTGAAGC				: 32

	*	1160	*	1180	*	1200	
LpPEPCb1 :	-----		-----		-----		-
LpPEPCb2 :	-----		-----		-----		-
LpPEPCb3 :		AGCGTCTGCGGCTGCGTGAGTCATAC-----					: 783
LpPEPCb4 :		AGCGTCTGCGGCTGCGTGAGTCATACATCACAACA-----					: 764
LpPEPCb5 :		AGCGTCTGCGGCTGCGTGAGTCATACATCACAACATTGAATGTTTGGCAAGCCATACACC					: 230
LpPEPCb6 :		AGCGTCTGCGGCTGCGTGAGTCATACATCACAACATTGAATGTTTGGCAAGCCATACACC					: 92

	*	1220	*	1240	*	1260	
LpPEPCb1 :	-----		-----		-----		-
LpPEPCb2 :	-----		-----		-----		-
LpPEPCb3 :	-----		-----		-----		-
LpPEPCb4 :	-----		-----		-----		-
LpPEPCb5 :		TGAAGCGGATAAGAGACCCTAGCTTCGAGGTGACACCGCAGCAGGCACCTCTGTCTGAAGG					: 290
LpPEPCb6 :		TGAAGCGGATAAGAGACCCTAGCTTCGAGGTGACACCGCAGCAGGCACCTCTGTCTGAAGG					: 152

	*	1280	*	1300	*	1320	
LpPEPCb1 :	-----		-----		-----		:
LpPEPCb2 :	-----		-----		-----		:
LpPEPCb3 :	-----		-----		-----		:
LpPEPCb4 :	-----		-----		-----		:
LpPEPCb5 :	AGTTCGCTGATGAGAAGGAGCCAGCTGAGCTGGTGCAACTGAACCGTGGGAGCGAGTACG						: 350
LpPEPCb6 :	AGTTCGCTGATGAGAAGGAGCCAGCTGAGCTGGTGCAACTGAACCGTGGGAGCGAGTACG						: 212

	*	1340	*	1360	*	1380	
LpPEPCb1 :	-----		-----		-----		:
LpPEPCb2 :	-----		-----		-----		:
LpPEPCb3 :	-----		-----		-----		:
LpPEPCb4 :	-----		-----		-----		:
LpPEPCb5 :	CCCCAGGCCTGGAGGACACCCTCATCCTTACCATGAAGGGTA-TTGCTGTGGAATGCAAA						: 409
LpPEPCb6 :	CCCCAGGCCTGGAGGACACCCTCATCCTTACCATGAAGGGTATTTGCTGTGGAATGCAAA						: 272

	*	1400	*	1420	*	1440	
LpPEPCb1 :	-----		-----		-----		:
LpPEPCb2 :	-----		-----		-----		:
LpPEPCb3 :	-----		-----		-----		:
LpPEPCb4 :	-----		-----		-----		:
LpPEPCb5 :	ACACAGGCTAGGCCAGTTTGCCTA-TTGGAAATAACTGTCATCCGTCAGATGGGGCGTGA						: 468
LpPEPCb6 :	ACACAGGCTAGGCCAGTTTGCCTATTTGGAAATAACTGTCATCCCGTCAGATGGGGCGTGA						: 331

	*	1460	*	1480	*	1500	
LpPEPCb1 :	-----		-----		-----		:
LpPEPCb2 :	-----		-----		-----		:
LpPEPCb3 :	-----		-----		-----		:
LpPEPCb4 :	-----		-----		-----		:
LpPEPCb5 :	ATATGTGTGTTCCCCAAATGCTAGTGAACCCTGGAGGCATTTTGGCCACTTACATGCCTT						: 528
LpPEPCb6 :	ATATGTGTGTTCCCCAAATGCTAGTGAACCCTGGAGGCA-TTGGCCACTTACATGCCTT						: 390

	*	1520	*	1540	*	1560	
LpPEPCb1 :	-----		-----		-----		:
LpPEPCb2 :	-----		-----		-----		:
LpPEPCb3 :	-----		-----		-----		:
LpPEPCb4 :	-----		-----		-----		:
LpPEPCb5 :	TTGGTTATGATGNAC-TTGATCTTAATGNCAAGGGTTGTTGAAGCCTGATCTAAATAAA						: 587
LpPEPCb6 :	TTGGTTATGGATGNACTTTGATCTTAATGCAAGGGTTGTTGAAGCCTGATCTAAATAAA						: 450

	*	1580	*	1600	*	1620	
LpPEPCb1 :	-----		-----		-----		:
LpPEPCb2 :	-----		-----		-----		:
LpPEPCb3 :	-----		-----		-----		:
LpPEPCb4 :	-----		-----		-----		:
LpPEPCb5 :	ATATGGAACAATGATATTCTGG-NGGATCTAATAATTTGCTTGGCTGTGGCATCGNAATA						: 646
LpPEPCb6 :	ATATGGAACAATGATATTCTGGTGGTCTCTTA						: 482

	*	1640	
LpPEPCb1 :	-----		:
LpPEPCb2 :	-----		:
LpPEPCb3 :	-----		:
LpPEPCb4 :	-----		:
LpPEPCb5 :	GNGATTTGGAGTNGTTTAAAC		: 666
LpPEPCb6 :	-----		:

Figure 47 Nucleotide sequence of LpPEPCc

LpPEPCc : AGCANTCTGTNCTTNCCANCAACCACGTTTTGTNCGAATACTTNCCGCTCGGCAACACCT : 60

LpPEPCc : GCACACTGAATATGGTCGGCATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTG : 120

LpPEPCc : GAGGCATAGAATCGCTCCGTGCAATTCCATGCATCTTTGNTTGGACACAGACAAGGNTTN : 180

LpPEPCc : ATNTTCCTGTATGNCCTTGNATTGNCCTCCACCNCACCCCNNTA : 224

Figure 48 Deduced amino acid sequence of LpPEPCc

LpPEPCc : XSXLXNHVLXEYXPLGNTCTLNMVGMNIGSRPSKRKPSGGIESLRAIPCIFXWTQTRXX : 60

LpPEPCc : XPVXLXFXSTXTP : 73

Figure 49 Nucleotide sequence of LpPEPCd

```

      *      20      *      40      *      60
LpPEPCd : GTTNCTGGAACNAAGGATCTTCTTGAAGGTGATCCCTACCTGAAGCAGCGGCTCCGCCTC : 60

      *      80      *      100     *      120
LpPEPCd : CGTGACGCGTACATCACCACCATGAACGTATGCCAGGCTACACATTGAAGCGGATCCGT : 120

      *      140     *      160     *      180
LpPEPCd : GACCCAGACTACCACGTCGCACTGCGGCCCCATCTTTCCAAGGAGGTTATGGACACAAGC : 180

      *      200     *      220     *      240
LpPEPCd : AAGCCGGCTTCCGAGCTTGTGACGCTGAACCCGGCCAGCGAGTACGCCCCGGGGCTGGAG : 240

      *      260     *      280     *      300
LpPEPCd : GACACCCTCATCTTGACCATGAAGGGCGTTGCTGCCGGTCTGCAAAACACCGGTTAGGGC : 300

      *      320     *      340     *      360
LpPEPCd : CAGGAGAGATGCCTGATCACCATCTTTTGTATCTTCATGATGATGCGATGTTTTTCTTT : 360

      *      380     *      400     *      420
LpPEPCd : AGTCGTTTGCGGTGGGCCTTATATCTCTCGGACGTAGCTGCATCTGTCTCCCTGCTCAGT : 420

      *      440     *      460     *      480
LpPEPCd : GAGGAATAATGGCGTTTCGCCCCAAGTATATTGATAAATAAAGGGAACCGATGTTAATTTTC : 480

      *      500     *      520
LpPEPCd : AGATTTGTTTGTAGTAATTGTTCTATTTATTTTGCGAAAAAAAAA : 527

```


Figure 50 Deduced amino acid sequence of LpPEPCd

* 20 * 40 * 60
LpPEPCd : VXGKDLLEGDPYLKQRLRLRDYITTMNVCQAYTLKRIRDPDYHVALRPHLSKEVMDTS : 60

* 80 *
LpPEPCd : KPASELVTLNPASEYAPGLEDTLILTMKGVAAGLQNTG : 98

Figure 51 Nucleotide sequence of LpPEPCe

```

      *           20           *           40           *           60
LpPEPCe : GTTACACGCGCAGTTTGCTTGTAGCAAGGNAGATGGCTGCTAACTTGTA CTTCTCTCAG : 60

      *           80           *           100          *           120
LpPEPCe : ATAGAAGATCTGATGTTTGAGCTCTCTATGTGGCGCTGCAGTGATGAACTTAGGGTCCGT : 120

      *           140          *           160           *           180
LpPEPCe : GCAGATGAAGTACATCTGTCCTCAAAAAAAAAAATCTGCAAAGCATTACATAGAGTTCTGG : 180

      *           200          *           220           *           240
LpPEPCe : AAGCAAGTTCCTCCAAATGAACCTTATCGTGTCACTTGGCGATGTCAGGGATAAACTG : 240

      *           260          *           280           *           300
LpPEPCe : TACTATACGCGCGAACGTTCTCGCCACATATTGACAACCTGGAATTTTCAGACATTCCAGAA : 300

      *           320          *           340           *           360
LpPEPCe : GNGTCAACTTTTACTAATGTTGAACTGTTTCTGGAACCTCTTGAGCTGTGCTACAGATCC : 360

      *           380          *           400           *           420
LpPEPCe : TTATCTTINCTGTGGNGACAAANCTATTGCTGANGGAAGCCTTCTTGATTCTNGCGNNCN : 420

      *           440          *
LpPEPCe : GNATCNACTTTGTGGGCTTACTCTNGCGAA : 450

```

Figure 52 Deduced amino acid sequence of LpPEPCe

LpPEPCe : VTRAVCLLARXMAANLYFSQIEDLMFELSMWRCSDELVRRADEVHLSSKKKSAKHYIEFW : 60

LpPEPCe : KQVPPNEPYRVILGDVRDKLYYTRERSRHILTTGISDIPEXSTFTNVELFLEPLELCYRS : 120

LpPEPCe : LSXCXDKXIAXGSLLDFXXXXTLWAYSXE : 150

Figure 53 Nucleotide sequence of LpPEPCf

LpPEPCf : GGGGTGGTGGCCCTNCTCACCTTGCCTNCCTGTCTCANCCACCAGNCACAATCAACGGAT : 60

LpPEPCf : CACTCCGGGTGACTGTTCAAGGTGAAGTTATTGAGCAGAGCTTTGGGGAGGAACACTTGT : 120

LpPEPCf : GCTTCAGGACGCTGCAGCGTTTCACAGCTGCTACTCTTGAGCATGGGATGCGTCCACCCA : 180

LpPEPCf : TTTCACCAAAGCCAGAGTGGCGAGCTCTTCTTGATGAGATGGCTGTGGTTGCAACTGAGG : 240

LpPEPCf : AATACCGGTCAATCGTCTTCCAAGAACCACGCTTCGTCGAGTATTTCCGCCTTGCAACAC : 300

LpPEPCf : CAGAGACAGAGTATGGCAGGATGAATATAGGAAGCAGGCCATCAAAGAGAAAACCAAGTG : 360

LpPEPCf : GTGGCATTGAATCACTCCGTGCAATTCCATGGATCTTCGCATGGACGCAGACACGGTTCC : 420

LpPEPCf : ACCTTCCAGTCTGGTTGGGCTTTGGTGGTGCATTCAAGCATATCCTCAAGAAGGACATCA : 480

LpPEPCf : GAAATTTCCATATGCTCCAGGAGATGTACAACGAGTGGCCATTTTTTCAGGGTCACGATCG : 540

LpPEPCf : ATCTTGTTGAGATGGTGTTCGCCAAGGGTAACCTGGCATTGCTGCCTTGTATGACAGGC : 600

LpPEPCf : TCCTGGTTTTCAGAGGAGCTACAGCCACTGGGTGACAAGCTGAGG : 644

Figure 54 Deduced amino acid sequence of LpPEPCf

LpPEPCf : GGGPXHLAXLSXPPXTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRF²⁰TAATLEHGMRPPI : 60⁴⁰

LpPEPCf : SPKPEWRALLDEMAVVATEEYRSIVFQEPRFVEYFRLATPETEYGRMNIGSRPSKRKPSG : 120⁸⁰

LpPEPCf : GIESLRAIPWIFAWTQTRFHL¹⁴⁰FPVWLGFGGAFKHILKKDIRNFHMLQEMYNEWPPFRVTID : 180¹⁶⁰

LpPEPCf : LVEMVFAKGNPGIAALYDRLLVSEELQPLGDKLR : 214²⁰⁰

Figure 55 Consensus contig nucleotide sequence of TrMDHa

```

      *      20      *      40      *      60
TrMDHa : GGCTTCTTAAAAACNCACTAAACTCTTTTCTATTGTTCTTATTCTTCGATCTATTTCCA : 60

      *      80      *      100     *      120
TrMDHa : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACCTGGTGTGCAGGACAAATTGGGTATGCT : 120

      *      140     *      160     *      180
TrMDHa : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 180

      *      200     *      220     *      240
TrMDHa : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTAAAATGGAGTTGGTGGAT : 240

      *      260     *      280     *      300
TrMDHa : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACCTGATGTGGTTGAGGCATGCACT : 300

      *      320     *      340     *      360
TrMDHa : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 360

      *      380     *      400     *      420
TrMDHa : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 420

      *      440     *      460     *      480
TrMDHa : GCTGCTGCAAACCTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 480

      *      500     *      520     *      540
TrMDHa : TTGAAGGAATATGCTCCATCCATTCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC : 540

      *      560     *      580     *      600
TrMDHa : CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAAGTTTCTGATGTGAAA : 600

      *      620     *      640     *      660
TrMDHa : AATGTTATAATATGGGGGAAATNATTCATCAACTCAATACCCTGNTGTNAACCACNCAAC : 660

      *
TrMDHa : CGTTAAAATCTCCT : 674

```

Figure 56 Deduced amino acid sequence of TrMDHa

TrMDHa : MAKDPVRVLVTGAAGQIGYALVPMIARGVMLGPDQPVILHMLDIPPAESLNGVKMELVD : 60

TrMDHa : AAFPLLKGVVATTDVVEACTGVNIAVMVGGFPRKEGMRKDVMTKNVSIYKSQASALEKH : 120

TrMDHa : AAANCKVLVVANPANTNALILKEYAPSIPEKNISALTRLDHNRALGQISERLNVEVSDVK : 180

TrMDHa : NVIIWGKXFINSIPXCXPXNR : 201

Figure 57 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHa

	*	20	*	40	*	60			
TrMDHa1	:	GINTTCTT	CNAAACNC	CTAAAT	TCTTTTCTATTG	TCTT	TTTCTTCGATCTATTTC	CA : 60	
TrMDHa2	:	-GCAT	CTATAAC	CTT	TNTCTNAG	CTCTATTG	TCTTATTTCCTTCGATCTATTTC	CA : 59	
TrMDHa3	:	-GCNTCTT	-AAAAC	-CACTAA	ACTCTTTTCTATTG	TCTTATTTCCTTCGATCTATTTC	CA : 57		
TrMDHa4	:	-GCATCTT	-AAAAC	-CACTAA	ACTCTTTTCTATTG	TCTTATTTCCTTCGATCTATTTC	CA : 57		
TrMDHa5	:	--CTTCTT	-NAAAC	-CACTAA	ACTCTTTTCTATTG	TCTTATTTCCTTCGATCTATTTC	CC : 55		
TrMDHa6	:	-----	CNTT	AAAAACNC	CACTAA	ACTCTTTTCTATTG	TCTTATTTCCTTCGATCTATTTC	CA : 54	
TrMDHa7	:	-----	-----	GCAT	TAAACTCTTTT	TATTGTTCTT	TTTCTTCGATCTATTTC	CC : 45	
TrMDHa8	:	-----	-----	GCAT	TAAACTCTTTT	TCTATTGTTCTT	TATTTCCTTCGATCTATTTC	CC : 45	
TrMDHa9	:	-----	-----	CACT	-AACTCTTTT	CTT	TTGTTCTT	TTTCTTCGATC-ATTTC	CC : 41
TrMDHa10	:	-----	-----	-----	TAAACTCTTT	TCTATTGTTCTT	TTTCTTCGATCTATTTC	CC : 41	
TrMDHa11	:	-----	-----	-----	AAACTCTTTT	TCTATTGTTCTT	TATTTCCTTCGATCTATTTC	CA : 41	

	*	80	*	100	*	120	
TrMDHa1	:	ATGGCCAAAGACCCAGTT	CGTGTCTT	GTCT	CTGGTGCTGCAGGACA	AGTTGGGTATGCT	: 120
TrMDHa2	:	ATGGCCAAAGACCCAGTT	CGTGTCTT	GTCT	CTGGTGCTGCAGGACA	AAATTGGGTATGCT	: 119
TrMDHa3	:	ATGGCCAAAGACCCAGTT	CGTGTCTT	GTCT	CTGGTGCTGCAGGACA	AAATTGGGTATGCT	: 117
TrMDHa4	:	ATGGCCAAAGACCCAGTT	CGTGTCTT	GTCT	CTGGTGCTGCAGGACA	AAATTGGGTATGCT	: 117
TrMDHa5	:	ATGGCCAAAGACCCAGTT	CGTGTCTT	GTCT	CTGGTGCTGCAGGACA	AGTTGGGTATGCT	: 115
TrMDHa6	:	ATGGCCAAAGACCCAGTT	CGTGTCTT	GTCT	CTGGTGCTGCAGGACA	AGTTGGGTATGCT	: 114
TrMDHa7	:	ATGGCC	-AAGACCCAGTT	CGTGTCTT	GTCT	CTGGTGCTGCAGGACA	AAATTGGGTATGCT : 104
TrMDHa8	:	ATGGCC	-AAGACCCAGTT	CGTGTCTT	GTCT	CTGGTGCTGCAGGACA	AAATTGGGTATGCT : 103
TrMDHa9	:	ATGGCC	-AAGACCCAGTT	CGTGTCTT	GTCT	CTGGTGCTGCAGGACA	AGTTGGGTATGCT : 99
TrMDHa10	:	ATGGCC	-AAGACCCAGTT	CGTGTCTT	GTCT	CTGGTGCTGCAGGACA	AAATTGGGTATGCT : 100
TrMDHa11	:	ATGGCCAAAGACCCAGTT	CGTGTCTT	GTCT	CTGGTGCTGCAGGACA	AAATTGGGTATGCT	: 101

	*	140	*	160	*	180	
TrMDHa1	:	CTTGTC	CCCTATGATT	GCTAGGGGAGT	GATGCTCGG	CCCTGACCAGC	CTGTGATCCTCCAC : 180
TrMDHa2	:	CTTGTC	CCCTATGATT	GCTAGGGGAGT	GATGCTCGG	CCCTGACCAGC	CTGTGATCCTCCAC : 179
TrMDHa3	:	CTTGTC	CCCTATGATT	GCTAGGGGAGT	GATGCTCGG	CCCTGACCAGC	CTGTGATCCTCCAC : 177
TrMDHa4	:	CTTGTC	CCCTATGATT	GCTAGGGGAGT	GATGCTCGG	CCCTGACCAGC	CTGTGATCCTCCAC : 177
TrMDHa5	:	CTTGTC	CCCTATGATT	GCTAGGGGAGT	GATGCTCGG	CCCTGACCAGC	CTGTGATCCTCCAC : 175
TrMDHa6	:	CTTGTC	CCCTATGATT	GCTAGGGGAGT	GATGCTCGG	CCCTGACCAGC	CTGTGATCCTCCAC : 174
TrMDHa7	:	CTTGTC	CCCTATGATT	GCTAGGGGAGT	GATGCTCGG	CCCTGACCAGC	CTGTGATCCTCCAC : 164
TrMDHa8	:	CTTGTC	CCCTATGATT	GCTAGGGGAGT	GATGCTCGG	CCCTGACCAGC	CTGTGATCCTCCAC : 163
TrMDHa9	:	CTTGTC	CCCTATGATT	GCTAGGGGAGT	GATGCTCGG	CCCTGACCAGC	CTGTGATCCTCCAC : 159
TrMDHa10	:	CTTGTC	CCCTATGATT	GCTAGGGGAGT	GATGCTCGG	CCCTGACCAGC	CTGTGATCCTCCAC : 160
TrMDHa11	:	CTTGTC	CCCTATGATT	GCTAGGGGAGT	GATGCTCGG	CCCTGACCAGC	CTGTGATCCTCCAC : 161

	*	200	*	220	*	240	
TrMDHa1	:	ATGCTTGACATT	CCACCTGCAG	CCGAATCACT	CAACGGTGTT	AAAAATGGAGTTGGTGGAT	: 202
TrMDHa2	:	ATGCTTGACATT	CCACCTGCAG	CCGAATCACT	CAACGGTGTT	AAAAATGGAGTTGGTGGAT	: 239
TrMDHa3	:	ATGCTTGACATT	CCACCTGCAG	CCGAATCACT	CAACGGTGTT	AAAAATGGAGTTGGTGGAT	: 237
TrMDHa4	:	ATGCTTGACATT	CCACCTGCAG	CCGAATCACT	CAACGGTGTT	AAAAATGGAGTTGGTGGAT	: 237
TrMDHa5	:	ATGCTTGACATT	CCACCTGCAG	CCGAATCACT	CAACGGTGTT	AAAAATGGAGTTGGTGGAT	: 235
TrMDHa6	:	ATGCTTGACATT	CCACCTGCAG	CCGAATCACT	CAACGGTGTT	AAAAATGGAGTTGGTGGAT	: 234
TrMDHa7	:	ATGCTTGACATT	CCACCTGCAG	CCGAATCACT	CAACGGTGTT	AAAAATGGAGTTGGTGGAT	: 224
TrMDHa8	:	ATGCTTGACATT	CCACCTGCAG	CCGAATCACT	CAACGGTGTT	AAAAATGGAGTTGGTGGAT	: 223
TrMDHa9	:	ATGCTTGACATT	CCACCTGCAG	CCGAATCACT	CAACGGTGTT	AAAAATGGAGTTGGTGGAT	: 219
TrMDHa10	:	ATGCTTGACATT	CCACCTGCAG	CCGAATCACT	CAACGGTGTT	AAAAATGGAGTTGGTGGAT	: 220
TrMDHa11	:	ATGCTTGACATT	CCACCTGCAG	CCGAATCACT	CAACGGTGTT	AAAAATGGAGTTGGTGGAT	: 221

	*	260	*	280	*	300		
TrMDHa1	:	-----					:	-
TrMDHa2	:	GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACCACTGATGTGGTTGAGGCATGCAC					:	299
TrMDHa3	:	GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACCACTGATGTGGTTGAGGCATGCAC					:	297
TrMDHa4	:	GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACCACTGATGTGGTTGAGGCATGCAC					:	297
TrMDHa5	:	GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACCACTGATGTGGTTGAGGCATGCAC					:	295
TrMDHa6	:	GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACCACTGATGTGGTTGAGGCATGCAC					:	294
TrMDHa7	:	GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACCACTGATGTGGTTGAGGCATGCAC					:	284
TrMDHa8	:	GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACCACTGATGTGGTTGAGGCATGCAC					:	283
TrMDHa9	:	GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACCACTGATGTGGTTGAGGCATGCAC					:	279
TrMDHa10	:	GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACCACTGATGTGGTTGAGGCATGCAC					:	280
TrMDHa11	:	GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACCACTGATGTGGTTGAGGCATGCAC					:	281

	*	320	*	340	*	360		
TrMDHa1	:	-----					:	-
TrMDHa2	:	GGGTCAATATTGCCGTTATGGTTGGCGGGTTCCTAGAAAAGAAGGTATGGAGAGGAAA					:	359
TrMDHa3	:	GGGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA					:	357
TrMDHa4	:	GGGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA					:	357
TrMDHa5	:	GGGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA					:	355
TrMDHa6	:	GGGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA					:	344
TrMDHa7	:	GGGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA					:	344
TrMDHa8	:	GGGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA					:	343
TrMDHa9	:	GGGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA					:	339
TrMDHa10	:	GGGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA					:	340
TrMDHa11	:	GGGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA					:	341

	*	380	*	400	*	420		
TrMDHa1	:	-----					:	-
TrMDHa2	:	GATGTGATGACAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT					:	419
TrMDHa3	:	GATGTGATGACAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT					:	417
TrMDHa4	:	GATGTGATGACAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT					:	417
TrMDHa5	:	GATGTGATGACAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT					:	415
TrMDHa6	:	-----					:	-
TrMDHa7	:	GATGTGATGACAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT					:	404
TrMDHa8	:	GATGTGATGACAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT					:	403
TrMDHa9	:	GATGTGATGACAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT					:	399
TrMDHa10	:	GATGTGATGACAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT					:	400
TrMDHa11	:	GATGTGATGACAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT					:	400

	*	440	*	460	*	480		
TrMDHa1	:	-----					:	-
TrMDHa2	:	GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC					:	479
TrMDHa3	:	GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC					:	477
TrMDHa4	:	GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC					:	477
TrMDHa5	:	GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC					:	475
TrMDHa6	:	-----					:	-
TrMDHa7	:	GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC					:	464
TrMDHa8	:	GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC					:	463
TrMDHa9	:	GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC					:	459
TrMDHa10	:	GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC					:	460
TrMDHa11	:	GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC					:	460

	*	500	*	520	*	540	
TrMDHa1	:	-----	:	-----	:	-----	:
TrMDHa2	:	TTGAAGGAATATGCTCCATCCATTTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC	:		:		: 539
TrMDHa3	:	TTGAAGGAATATGCTCCATCCATTTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC	:		:		: 537
TrMDHa4	:	TTGAAGGAATATGCTCCATCCATTTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC	:		:		: 537
TrMDHa5	:	TTGAAGGAATATGCTCCATCCATTTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC	:		:		: 535
TrMDHa6	:	-----	:	-----	:	-----	:
TrMDHa7	:	TTGAAGGAATATGCTCCATCCATTTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC	:		:		: 524
TrMDHa8	:	TTGAAGGAATATGCTCCATCCATTTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC	:		:		: 523
TrMDHa9	:	TTGAAGGAATATGCTCCATCCATTTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC	:		:		: 519
TrMDHa10	:	TTGAAGGAATATGCTCCATCCATTTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC	:		:		: 520
TrMDHa11	:	TTGAAGGAATATGCTCCATTCATTTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC	:		:		: 520

	*	560	*	580	*	600	
TrMDHa1	:	-----	:	-----	:	-----	:
TrMDHa2	:	CATAACAGGGCACTTTGGTCA-----	:		:		: 559
TrMDHa3	:	CATAACAGGGCACTAGGTCAAATTTCTGAA-----	:		:		: 567
TrMDHa4	:	CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAA-----	:		:		: 575
TrMDHa5	:	CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAAGTTTCTGATGTGAAA	:		:		: 595
TrMDHa6	:	-----	:	-----	:	-----	:
TrMDHa7	:	CATAACAGGGCACTAGGTCAAATTTCTGAAAGAC-----	:		:		: 558
TrMDHa8	:	CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAAGTTTCTGATGTGAAA	:		:		: 583
TrMDHa9	:	CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAAGTTTCTGATGTGAG--	:		:		: 577
TrMDHa10	:	CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAAGTTTCTGATGTGAAA	:		:		: 580
TrMDHa11	:	CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAAGTTTCTGATGTGAAA	:		:		: 580

	*	620	*	640	*	660	
TrMDHa1	:	-----	:	-----	:	-----	:
TrMDHa2	:	-----	:	-----	:	-----	:
TrMDHa3	:	-----	:	-----	:	-----	:
TrMDHa4	:	-----	:	-----	:	-----	:
TrMDHa5	:	AATGTTAT-A-AT-----	:		:		: 606
TrMDHa6	:	-----	:	-----	:	-----	:
TrMDHa7	:	-----	:	-----	:	-----	:
TrMDHa8	:	AATGTTATAATCTGGG-----	:		:		: 599
TrMDHa9	:	-----	:	-----	:	-----	:
TrMDHa10	:	AATGTTATAATCTG-----	:		:		: 594
TrMDHa11	:	AATGTTAT-ATATGGGGGAAATNATTCATCAACTCAATACCCTGNTGTNAACCACNCAAC	:		:		: 639

	*		
TrMDHa1	:	-----	:
TrMDHa2	:	-----	:
TrMDHa3	:	-----	:
TrMDHa4	:	-----	:
TrMDHa5	:	-----	:
TrMDHa6	:	-----	:
TrMDHa7	:	-----	:
TrMDHa8	:	-----	:
TrMDHa9	:	-----	:
TrMDHa10	:	-----	:
TrMDHa11	:	CGTTAAAATCTCCT	: 653

Figure 58 Consensus contig nucleotide sequence of TrMDHb

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      *           20           *           40           *           60
TrMDHb : TTCTCCCANAAATCNNGAAANCGCCCANACATCACACAACATAACACCTTACTCTNCTTTC : 60

      *           80           *           100          *           120
TrMDHb : TCTCTNAACAAAACTGTTCTTCCTCTCTTAATCTTCCCTGTTTCGATTCCCTTCCATTTCT : 120

      *           140          *           160           *           180
TrMDHb : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCCTGCAGGGCAAATTGGT : 180

      *           200          *           220           *           240
TrMDHb : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 240

      *           260          *           280           *           300
TrMDHb : CTTCACATGCTTGATATTCTCCAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 300

      *           320          *           340           *           360
TrMDHb : GTCGATGCTGCATTTCCTTCTTAAAGGTGTTGTTGCTACAACCTGATGTTGTTGAAGCA : 360

      *           380          *           400           *           420
TrMDHb : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 420

      *           440          *           460           *           480
TrMDHb : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 480

      *           500          *           520           *           540
TrMDHb : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCAGCAAACACCAATGCA : 540

      *           560          *           580           *           600
TrMDHb : TTGATCTTGAAGGAATTTGCTCCATCTATTCAGAGAAAAACATTTCTTGTGTTGACTAGA : 600

      *           620          *           640           *           660
TrMDHb : CTTGATCACAAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAAGTTTCTGAT : 660

      *           680          *           700           *           720
TrMDHb : GTAAAGAATGTCATTATCTGGGGTAATCATTCATCAACTCAGTATCCTGATGTCAACCAT : 720

      *           740          *           760           *           780
TrMDHb : GCAACTGTTAACACCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGTCTTCTGATGACGCC : 780

      *           800          *           820           *           840
TrMDHb : TGGTTGAATGGAGAATTTCATATCTACCGTTCAACAACGTGGTGCTGCAATTATTAAGGCT : 840

      *           860          *           880           *           900
TrMDHb : AGAAAGCTTTCAAGCGCACTATCCGCTGCTAGCGCTGCTTGCGACCACATTCGCGATTGG : 900

      *           920          *           940           *           960
TrMDHb : GTTCTTGGAACCTCCCCAGGGCACCTTCGTTTCAATGGGAGTGATTCTGATGGTTCTTAC : 960

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* 980 * 1000 * 1020
TrMDHb : AACGTACCAGCTGGACTCATCTATTCATTCCCTGTCACCACTGCTAATGGGGAATGGAAA : 1020

* 1040 * 1060 * 1080
TrMDHb : ATTGTTCAAGGACTTTCAATTGACGAGTTCTCAAGGAAGAAGTTGGACTTGACAGCTGAA : 1080

* 1100 *
TrMDHb : GAGTTATCCGAGGAAAAGAGTTTGGCATACT : 1111

Figure 59 Deduced amino acid sequence of TrMDHb

TrMDHb : * 20 * 40 * 60
 MAKDPVRVLVTGAAGQIGYALVPMIARGVMLGPDQPVILHMLDIPPAESLNGVKMELVD : 60

TrMDHb : * 80 * 100 * 120
 AAFPLLKGVVATTDVVEACTGVNIAVMVGGFPRKEGMRKDVMSKNVSIYKSQASALEKH : 120

TrMDHb : * 140 * 160 * 180
 AAANCKVLVVANPANTNALILKEFAPSIPEKNISCLTRLDHNRALGQISERLNVQVSDVK : 180

TrMDHb : * 200 * 220 * 240
 NVIIWGNHSSSQYPDVNHATVNTPAGEKPVRELVSDDAWLNGEFISTVQORGAAIIKARK : 240

TrMDHb : * 260 * 280 * 300
 LSSALSAASAACDHIRDWVLGTPQGTFFVSMGVSDGSYNVPAGLIYSFPVTTANGWKIV : 300

TrMDHb : * 320
 QGLSIDEFSRKKLDLTAEEELSEEKSLAY : 328

		*	80	*	100	*	120	
TrMDHb1	:	TCT	---	AAA	GAAA	ACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	GATTCCTTCCAGTTCT	: 104
TrMDHb2	:	TCT	---	AAA	GAAA	ACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	GATTCCTTCCAGTTCT	: 102
TrMDHb3	:	TNA	---	AAC	AAAA	ACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	CGATTCCTTCCATTCT	: 94
TrMDHb4	:	TCT	:	NAA	CAAA	AGCTATTCTTCACTCTTAATCTTCCCTGTTT	CGATTCCTTCCGTTCT	: 91
TrMDHb5	:	TCT	:	NAA	CAAA	AGCTATTCTTCACTCTTAATCTTCCCTGTTT	GATTCCTTCCGTTCT	: 91
TrMDHb6	:	TCT	---	NAA	GAAA	ACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	CGATTCCTTCCGGTCT	: 84
TrMDHb7	:	TNN	---	AAC	AAAA	ACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	CGATTCCTTCCGTTCT	: 85
TrMDHb8	:	TCT	:	NNA	CAAA	AACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	CGATTCCTTCCGTTCT	: 84
TrMDHb9	:	TCT	---	AAC	AAAA	ACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	CGATTCCTTCCATTCT	: 72
TrMDHb10	:	TCTCA	:	AAC	AAA	ACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	CGATTCCTTCCATTCT	: 78
TrMDHb11	:	TCTCTNAAC	:	AAA	ACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	CGATTCCTTCCAGTTCT		: 80
TrMDHb12	:	TCTCT	:	NAA	GAAA	ACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	CGATTCCTTCCATTCT	: 81
TrMDHb13	:	TCT	:	NAA	CAAA	AACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	CGATTCCTTCCGTTCT	: 75
TrMDHb14	:	TNC	---	AAA	AAAA	ACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	CGATTCCTTCCATTCT	: 71
TrMDHb15	:	TCTCT	:	AAA	GAAA	ACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	CGATTCCTTCCATTCT	: 79
TrMDHb16	:	TCTCTNAAC	:	AAA	ACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	CGATTCCTTCCGTTCT		: 78
TrMDHb17	:	TCT	:	CAA	ACAAA	AACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	CGATTCCTTCCATTCT	: 76
TrMDHb18	:	TCTCT	:	CAAC	AAA	ACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	GATTCCTTCCGTTCT	: 74
TrMDHb19	:	TCT	:	NNA	CAAA	AACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	CGATTCCTTCCATTCT	: 70
TrMDHb20	:	TNA	---	AAC	AAAA	ACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	CGATTCCTTCCATTCT	: 63
TrMDHb21	:	CTCTNAAC	:	AAA	AACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	GATTCCTTCCGTTCT		: 63
TrMDHb22	:	TCT	:	NAA	CAAA	AACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	CGATTCCTTCCATTCT	: 59
TrMDHb23	:	-----	:	CAAA	AACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	CGATTCCTTCCGTTCT		: 51
TrMDHb24	:	-----	:	AAA	AACTGTTCTTCCTCTCTTAATCTTCCCTGTTT	CGATTCCTTCCGTTCT		: 49
TrMDHb25	:	-----	:	GNN	TCTTCCTCTCTTAATCTTCCCTGTTT	GATTCCTTCCAGTTCT		: 46
TrMDHb26	:	-----	:	SGT	TCTTCCTCTCTTAATCTTCCCTGTTT	CGATTCCTTCCATTCT		: 44
TrMDHb27	:	-----	:	TTCC	TCTCTCTTAATCTTCCCTGTTT	GATTCCTTCCGTTCT		: 39
TrMDHb28	:	-----	:					: -
TrMDHb29	:	-----	:					: -
TrMDHb30	:	-----	:					: -
TrMDHb31	:	-----	:					: -
TrMDHb32	:	-----	:					: -

	*	140	*	160	*	180	
TrMDHb1	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 164
TrMDHb2	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 162
TrMDHb3	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 154
TrMDHb4	:	TCAGGCAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 151
TrMDHb5	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 151
TrMDHb6	:	TCAGGCAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 144
TrMDHb7	:	TCAGGCAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 145
TrMDHb8	:	TCAGGCAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 144
TrMDHb9	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 132
TrMDHb10	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 138
TrMDHb11	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 140
TrMDHb12	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 141
TrMDHb13	:	TCAGGCAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 135
TrMDHb14	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 131
TrMDHb15	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 139
TrMDHb16	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 138
TrMDHb17	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 136
TrMDHb18	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 134
TrMDHb19	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 130
TrMDHb20	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 123
TrMDHb21	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 123
TrMDHb22	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 119
TrMDHb23	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 110
TrMDHb24	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 109
TrMDHb25	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 106
TrMDHb26	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 103
TrMDHb27	:	TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT					: 97
TrMDHb28	:	-----					: -
TrMDHb29	:	-----					: -
TrMDHb30	:	-----					: -
TrMDHb31	:	-----					: -
TrMDHb32	:	-----					: -

TrMDHb1 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 224
TrMDHb2 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 222
TrMDHb3 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 214
TrMDHb4 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 211
TrMDHb5 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 211
TrMDHb6 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 204
TrMDHb7 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 205
TrMDHb8 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 204
TrMDHb9 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 192
TrMDHb10 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198
TrMDHb11 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 200
TrMDHb12 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 201
TrMDHb13 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 195
TrMDHb14 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 191
TrMDHb15 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199
TrMDHb16 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198
TrMDHb17 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 196
TrMDHb18 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 194
TrMDHb19 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 190
TrMDHb20 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183
TrMDHb21 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183
TrMDHb22 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 179
TrMDHb23 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 170
TrMDHb24 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169
TrMDHb25 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 166
TrMDHb26 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163
TrMDHb27 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 157
TrMDHb28 : -----GGGGAGTGATGCTTGGTCCTGAT-----NACCTGTGATC : 34
TrMDHb29 : ----- : -
TrMDHb30 : ----- : -
TrMDHb31 : ----- : -
TrMDHb32 : ----- : -

	*	260	*	280	*	300	
TrMDHb1	:	CTACACATGCTTGATATTCCACC	GCAGCAGAGTCATTGAATGGAGT	TAAGATGGAGATG	:	284	
TrMDHb2	:	CTACACATGCTTGATATTCCACC	GCAGCAGAGTCATTGAATGGAGT	TAAGATGGAGTTG	:	282	
TrMDHb3	:	CTTCACATGCTTGATATCCCTCCAGCAGCAGAGTCATTGAATGGAGT	TAAATGGAGTTG	:	274		
TrMDHb4	:	CTTCACATGCTTGATATCCCTCCAGCAGCAGAGTCATTGAATGGAGT	TAAATGGAGTTG	:	271		
TrMDHb5	:	CTTCACATGCTTGATATTCCCTCCAGCAGCAGAGTCATTGAATGGAGT	TAAGATGGAGTTG	:	271		
TrMDHb6	:	CTTCACATGCTTGATATCCCTCCAGCAGCAGAGTCATTGAATGGAGT	TAAATGGAGTTG	:	264		
TrMDHb7	:	CTTCACATGCTTGATATCCCTCCAGCAGCAGAGTCATTGAATGGAGT	TAAATGGAGTTG	:	265		
TrMDHb8	:	CTTCACATGCTTGATATCCCTCCAGCAGCAGAGTCATTGAATGGAGT	TAAATGGAGTTG	:	264		
TrMDHb9	:	CTTGACATGCTTGATATTCTCAGNAGNAGAGT	NATTGAATGGAGT	TAAATGGAGTTG	:	252	
TrMDHb10	:	CTACACATGCTTGATATTCCACC	GCAGCAGAGTCATTGAATGGAGT	TAAGATGGAGTTG	:	258	
TrMDHb11	:	CTTCACATGCTTGATATTCCCTCCAGCAGCAGAGTCATTGAATGGAGT	TAAGATGGAGTTG	:	260		
TrMDHb12	:	CTACACATGCTTGATATTCCACC	GCAGCAGAGTCATTGAATGGAGT	TAAGATGGAGTTG	:	261	
TrMDHb13	:	CTTCACATGCTTGATATCCCTCCAGCAGCAGAGTCATTGAATGGAGT	TAAATGGAGTTG	:	255		
TrMDHb14	:	CTTCACATGCTTGATATTCCCTCCAGCAGCAGAGTCATTGAATGGAGT	TAAATGGAGTTG	:	251		
TrMDHb15	:	CTACACATGCTTGATATTCCACC	GCAGCAGAGTCATTGAATGGAGT	TAAGATGGAGTTG	:	259	
TrMDHb16	:	CTACACATGCTTGATATTCCACC	GCAGCAGAGTCATTGAATGGAGT	TAAGATGGAGTTG	:	258	
TrMDHb17	:	CTTCACATGCTTGATATTCCCTCCAGCAGCAGAGTCATTGAATGGAGT	TAAATGGAGTTG	:	256		
TrMDHb18	:	CTTCACATGCTTGATATTCCCTCCAGCAGCAGAGTCATTGAATGGAGT	TAAGATGGAGTTG	:	254		
TrMDHb19	:	CTTCACATGCTTGATATTCCCTCCAGCAGCAGAGTCATTGAATGGAGT	TAAATGGAGTTG	:	250		
TrMDHb20	:	CTTCACATGCTTGATATTCCCTCCAGCAGCAGAGTCATTGAATGGAGT	TAAATGGAGTTG	:	243		
TrMDHb21	:	CTTCACATGCTTGATATTCCCTCCAGCAGCAGAGTCATTGAATGGAGT	TAAGATGGAGTTG	:	243		
TrMDHb22	:	CTTCACATGCTTGATATTCCCTCCAGCAGCAGAGTCATTGAATGGAGT	TAAATGGAGTTG	:	239		
TrMDHb23	:	CTACACATGCTTGATATTCCACC	GCAGCAGAGTCATTGAATGGAGT	TAAGATGGAGTTG	:	230	
TrMDHb24	:	CTACACATGCTTGATATTCCACC	GCAGCAGAGTCATTGAATGGAGT	TAAGATGGAGTTG	:	229	
TrMDHb25	:	CTTCACATGCTTGATATTCCCTCCAGCAGCAGAGTCATTGAATGGAGT	TAAGATGGAGTTG	:	226		
TrMDHb26	:	CTTCACATGCTTGATATTCCCTCCAGCAGCAGAGTCATTGAATGGAGT	TAAATGGAGTTG	:	223		
TrMDHb27	:	CTTCACATGCTTGATATTCTCCAGCAGCAGAGTCATTGAATGGAGT	TAAGATGGAGTTG	:	217		
TrMDHb28	:	CTTNCATGCTTGATATCCCTCCAGCAGCAGAGTCATTGAATGGAGT	TAAATGGAGTTG	:	93		
TrMDHb29	:	-----NTATTCCCTNCCGCAGCNGAGT	NTTGAATGGAG	TAAGATGGAGTTG	:	45	
TrMDHb30	:	-----TATTCCTCCGCAGCAGAGT	NTTGAATGGAG	TAAGATGGAGTTG	:	43	
TrMDHb31	:	-----			:	-	
TrMDHb32	:	-----			:	-	

	*	320	*	340	*	360		
TrMDHb1	:	GTCGATGCTGCTGATTNNCACTTCTTAAAGGCGANGCTGCT					:	323
TrMDHb2	:	GTCGATGCTGCATTTCCACTTCTTAAAGGTGCTGCTACAACTGATGATGCGAAGCA					:	342
TrMDHb3	:	GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	334
TrMDHb4	:	GTGGATGCTGCATTTCCACTTCTTAAAGGCGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	331
TrMDHb5	:	GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	331
TrMDHb6	:	GTGGATGCTGCATTTCCACTTCTTAAAGGCGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	324
TrMDHb7	:	GTGGATGCTGCATTTCCACTTCTTAAAGGCGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	325
TrMDHb8	:	GTGGATGCTGCATTTCCACTTCTTAAAGGCGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	324
TrMDHb9	:	GGCGATGCTGCTGATTNNCACTTCTTAAAGGCGCTGCTACCACTGATGCTGCGAAGCA					:	312
TrMDHb10	:	GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	318
TrMDHb11	:	GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	320
TrMDHb12	:	GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	321
TrMDHb13	:	GTGGATGCTGCATTTCCACTTCTTAAAGGCGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	315
TrMDHb14	:	GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	311
TrMDHb15	:	GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	319
TrMDHb16	:	GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	318
TrMDHb17	:	GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	316
TrMDHb18	:	GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	314
TrMDHb19	:	GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	310
TrMDHb20	:	GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	303
TrMDHb21	:	GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	303
TrMDHb22	:	GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	299
TrMDHb23	:	GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	290
TrMDHb24	:	GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	289
TrMDHb25	:	GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	286
TrMDHb26	:	GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	283
TrMDHb27	:	GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	277
TrMDHb28	:	GTGGATGCTGCATTTCCACTTCTTAAAGGCTTGTGTTGCTACAACTGATGTTGTTGAAGCA					:	153
TrMDHb29	:	GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	105
TrMDHb30	:	GTCGATGCTGCATTTCCCTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA					:	102
TrMDHb31	:	-----					:	-
TrMDHb32	:	-----					:	-

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TrMDHb1 : ----- : 350
TrMDHb2 : TNNCTGG----- : 394
TrMDHb3 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 391
TrMDHb4 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 391
TrMDHb5 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 384
TrMDHb6 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 385
TrMDHb7 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 384
TrMDHb8 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 333
TrMDHb9 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 378
TrMDHb10 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 380
TrMDHb11 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 381
TrMDHb12 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 375
TrMDHb13 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 371
TrMDHb14 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 379
TrMDHb15 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 378
TrMDHb16 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 376
TrMDHb17 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 374
TrMDHb18 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 370
TrMDHb19 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 363
TrMDHb20 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 363
TrMDHb21 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 359
TrMDHb22 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 350
TrMDHb23 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 349
TrMDHb24 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 346
TrMDHb25 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 343
TrMDHb26 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 337
TrMDHb27 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 213
TrMDHb28 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 165
TrMDHb29 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 162
TrMDHb30 : TGCCTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 4
TrMDHb31 : -----CGAG : 4
TrMDHb32 : -----NNNN : 4

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	*	440	*	460	*	480		
TrMDHb1	:	-----					:	-
TrMDHb2	:	-----					:	-
TrMDHb3	:	AGGAAGGATGTGATGCTAAGAACTGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	454
TrMDHb4	:	AGGAAGGATGTGATGCTAAGAACTGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	451
TrMDHb5	:	AGGAAGGATGTGATGCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	451
TrMDHb6	:	AGGAAGGATGTGATGCTAAGAACTGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	444
TrMDHb7	:	AGGAAGGATGTGATGCTAAGAACTGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	445
TrMDHb8	:	AGGAAGGATGTGATGCTAAGAACTGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	444
TrMDHb9	:	-----					:	-
TrMDHb10	:	AGGAAGGATGTGATGCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	438
TrMDHb11	:	AGGAAGGATGTGATGCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	440
TrMDHb12	:	AGGAAGGATGTGATGCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	441
TrMDHb13	:	AGGAAGGATGTGATGCTAAGAACTGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	435
TrMDHb14	:	AGGAAGGATGTGATGCTAAGAACTGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	431
TrMDHb15	:	AGGAAGGATGTGATGCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	439
TrMDHb16	:	AGGAAGGATGTGATGCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	438
TrMDHb17	:	AGGAAGGATGTGATGCTAAGAACTGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	436
TrMDHb18	:	AGGAAGGATGTGATGCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	434
TrMDHb19	:	AGGAAGGATGTGATGCTAAGAACTGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	430
TrMDHb20	:	AGGAAGGATGTGATGCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	423
TrMDHb21	:	AGGAAGGATGTGATGCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	423
TrMDHb22	:	AGGAAGGATGTGATGCTAAGAACTGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	419
TrMDHb23	:	AGGAAGGATGTGATGCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	410
TrMDHb24	:	AGGAAGGATGTGATGCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	409
TrMDHb25	:	AGGAAGGATGTGATGCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	406
TrMDHb26	:	AGGAAGGATGTGATGCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	403
TrMDHb27	:	AGGAAGGATGTGATGCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	397
TrMDHb28	:	AGGAAGGATGTGATGCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	273
TrMDHb29	:	AGGAAGGATGTGATGCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	225
TrMDHb30	:	AGGAAGGATGTGATGCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	222
TrMDHb31	:	AGGAAGGATGTGATGCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	64
TrMDHb32	:	NNGNANGNNGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA					:	64

* 500 *

520

* 540

TrMDHb1 : ----- : -
TrMDHb2 : ----- : -
TrMDHb3 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAAATACCAATGCA : 514
TrMDHb4 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAAATACCAATGCA : 511
TrMDHb5 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAAATACCAATGCA : 510
TrMDHb6 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAAATACCAATGCA : 504
TrMDHb7 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAAATACCAATGCA : 505
TrMDHb8 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAAATACCAATGCA : 504
TrMDHb9 : ----- : -
TrMDHb10 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAAACACCAATGCA : 498
TrMDHb11 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAAACACCAATGCA : 499
TrMDHb12 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAAACACCAATGCA : 501
TrMDHb13 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAAATACCAATGCA : 495
TrMDHb14 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGG----- : 462
TrMDHb15 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAAACACCAATGCA : 499
TrMDHb16 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAAACACCAATGCA : 498
TrMDHb17 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAAATACCAATGCA : 496
TrMDHb18 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAAACACCAATGCA : 493
TrMDHb19 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAAATACCAATGCA : 490
TrMDHb20 : AAGCATGCTG----- : 433
TrMDHb21 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAAACACCAATGCA : 483
TrMDHb22 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAAATACCAATGCA : 479
TrMDHb23 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAAACACCAATGCA : 470
TrMDHb24 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAAACACCAATGCA : 469
TrMDHb25 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAAACACCAATGCA : 466
TrMDHb26 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAAATACCAATGCA : 463
TrMDHb27 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAAACACCAATGCA : 457
TrMDHb28 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAAATACCAATGCA : 333
TrMDHb29 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAAACACCAATGCA : 285
TrMDHb30 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAAACACCAATGCA : 282
TrMDHb31 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAAACACCAATGCA : 124
TrMDHb32 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAAACACCAATGCA : 124

* 560 * 580 * 600

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TrMDHb1 : ----- : -
TrMDHb2 : ----- : -
TrMDHb3 : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGCTTTGACTAGA : 574
TrMDHb4 : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGCTTTGACTAGA : 571
TrMDHb5 : TTGATCTTGAAGGAATCTGGCT----- : 531
TrMDHb6 : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGCTTTGACTAGA : 564
TrMDHb7 : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGCTTTGACTAGA : 565
TrMDHb8 : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGCTTTGACTAGA : 564
TrMDHb9 : ----- : -
TrMDHb10 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGTTTGACTAGA : 558
TrMDHb11 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGTTTGACTAGA : 559
TrMDHb12 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGTTTGACTAGA : 561
TrMDHb13 : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGCTTTGACTAGA : 555
TrMDHb14 : ----- : -
TrMDHb15 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGTTTGACTAGA : 559
TrMDHb16 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGTTTGACTAGA : 558
TrMDHb17 : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGCTTTG----- : 550
TrMDHb18 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGTTTGACTAGA : 553
TrMDHb19 : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGCTTTGACTAGA : 550
TrMDHb20 : ----- : -
TrMDHb21 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGTTTGACTAGA : 543
TrMDHb22 : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGCTTTGACTAGA : 539
TrMDHb23 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGTTTGACTAGA : 530
TrMDHb24 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGTTTGACTAGA : 529
TrMDHb25 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGTTTGACTAGA : 526
TrMDHb26 : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGCTTTGACTAGA : 523
TrMDHb27 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGTTTGACTAGA : 517
TrMDHb28 : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGCTTTGACTAGA : 393
TrMDHb29 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGTTTGACTAGA : 345
TrMDHb30 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGTTTGACTAGA : 342
TrMDHb31 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGTTTGACTAGA : 184
TrMDHb32 : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTGGTTTGACTAGA : 184

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	*	620	*	640	*	660		
TrMDHb1	:	-----					:	-
TrMDHb2	:	-----					:	-
TrMDHb3	:	CTTGATCACAA-----					:	585
TrMDHb4	:	CTTGATCACAAACAGGGCATTGG-----					:	593
TrMDHb5	:	-----					:	-
TrMDHb6	:	CTTGATCAC-----					:	573
TrMDHb7	:	CTTGATCACAAACAGGGCATTGGGCCAAATTTCTGAAAG-----					:	603
TrMDHb8	:	CTTGATCACAAACAGGGCATTGGGCCAAATTTCT-----					:	597
TrMDHb9	:	-----					:	-
TrMDHb10	:	CTTGATCAC-----					:	567
TrMDHb11	:	CTTGATCAC-----					:	569
TrMDHb12	:	CTTGATCACAAACAGGGCATTGGGCCAAATTT-----					:	592
TrMDHb13	:	CTTGATCACAAACAGGGCATTGGGCCAAATT-----					:	585
TrMDHb14	:	-----					:	-
TrMDHb15	:	CTTGATCACAAACAG-----					:	573
TrMDHb16	:	CTTGATCACAAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAAT-----					:	603
TrMDHb17	:	-----					:	-
TrMDHb18	:	CTTGATCACAAACAGGGCATTGGGCCAAATTTCTGAAAG-----					:	591
TrMDHb19	:	CTTGATCACAAACAGGGCATTG-----					:	571
TrMDHb20	:	-----					:	-
TrMDHb21	:	CTTGATCACAAACAGGGCATTGGGCCAAATTTCTGAAAGATTG-----					:	585
TrMDHb22	:	CTTGATCACAAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATATTC AAGTTTCTGAT					:	599
TrMDHb23	:	CTTGATCACAAACAGGGCATTGGGCCAAATTTCTGAAAG-----					:	568
TrMDHb24	:	CTTGATCACAAACAGGGCATTGGGCCAAAT-----					:	558
TrMDHb25	:	CTTGATCACAAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAAGTTTCTGAT					:	586
TrMDHb26	:	CTTGATCACAAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATATTC AAGTTTCTGAT					:	583
TrMDHb27	:	CTTGATCACAAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAAGTTTC-----					:	573
TrMDHb28	:	CTTGATCACAAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATATTC AAGTTTCTGAT					:	453
TrMDHb29	:	CTTGATCACAAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAAGTTTCTGAT					:	405
TrMDHb30	:	CTTGATCACAAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAAGTTTCTGAT					:	402
TrMDHb31	:	CTTGATCACAAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAAGTTTCTGAT					:	244
TrMDHb32	:	CTTGATCACAAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAAGTTTCTGAT					:	244

	*	680	*	700	*	720		
TrMDHb1	:	-----					:	-
TrMDHb2	:	-----					:	-
TrMDHb3	:	-----					:	-
TrMDHb4	:	-----					:	-
TrMDHb5	:	-----					:	-
TrMDHb6	:	-----					:	-
TrMDHb7	:	-----					:	-
TrMDHb8	:	-----					:	-
TrMDHb9	:	-----					:	-
TrMDHb10	:	-----					:	-
TrMDHb11	:	-----					:	-
TrMDHb12	:	-----					:	-
TrMDHb13	:	-----					:	-
TrMDHb14	:	-----					:	-
TrMDHb15	:	-----					:	-
TrMDHb16	:	-----					:	-
TrMDHb17	:	-----					:	-
TrMDHb18	:	-----					:	-
TrMDHb19	:	-----					:	-
TrMDHb20	:	-----					:	-
TrMDHb21	:	-----					:	-
TrMDHb22	:	GTAAAGAATGT-----					:	-
TrMDHb23	:	-----					:	610
TrMDHb24	:	-----					:	-
TrMDHb25	:	GTAAAGAATGTCATTATCTGGGGTAATCATTCATCAACTCAGTATCC					:	-
TrMDHb26	:	TGATGTCAACCAT-----					:	646
TrMDHb27	:	-----					:	-
TrMDHb28	:	GTAAAGAATGTCATTATCTGGGGTAATCATTCATCAACTCAGTATCC					:	-
TrMDHb29	:	TGATGTCAACCAT-----					:	513
TrMDHb30	:	GTAAAGAATGTCATTATCTGGGTAATCATTCATCAACTCAGTATCC					:	-
TrMDHb31	:	TGATGTCAACCAT-----					:	465
TrMDHb32	:	GTAAAGAATGTCATTATCTGGGGTAATCATTCATCAACTCAGTATCC					:	-
	:	TGATGTCAACCAT-----					:	462
	:						:	304
	:						:	304

	*	740	*	760	*	780	
TrMDHb1	:	-----					-
TrMDHb2	:	-----					-
TrMDHb3	:	-----					-
TrMDHb4	:	-----					-
TrMDHb5	:	-----					-
TrMDHb6	:	-----					-
TrMDHb7	:	-----					-
TrMDHb8	:	-----					-
TrMDHb9	:	-----					-
TrMDHb10	:	-----					-
TrMDHb11	:	-----					-
TrMDHb12	:	-----					-
TrMDHb13	:	-----					-
TrMDHb14	:	-----					-
TrMDHb15	:	-----					-
TrMDHb16	:	-----					-
TrMDHb17	:	-----					-
TrMDHb18	:	-----					-
TrMDHb19	:	-----					-
TrMDHb20	:	-----					-
TrMDHb21	:	-----					-
TrMDHb22	:	-----					-
TrMDHb23	:	-----					-
TrMDHb24	:	-----					-
TrMDHb25	:	GCAACTGTTAACACCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGT				TCTGATGACGCC	706
TrMDHb26	:	-----					-
TrMDHb27	:	-----					-
TrMDHb28	:	GCAACTGTTAACACCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGT				TCTGATGACGCC	562
TrMDHb29	:	GCAACTGTTAACACCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGT				TCTGATGACGCC	515
TrMDHb30	:	GCAACTGTTAACACCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGT				TCTGATGACGCC	522
TrMDHb31	:	GCAACTGTTAACACCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGT				TCTGATGACGCC	364
TrMDHb32	:	GCAACTGTTAACACCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGT				TCTGATGACGCC	364

	*	800	*	820	*	840	
TrMDHb1	:	-----		-----		-----	-
TrMDHb2	:	-----		-----		-----	-
TrMDHb3	:	-----		-----		-----	-
TrMDHb4	:	-----		-----		-----	-
TrMDHb5	:	-----		-----		-----	-
TrMDHb6	:	-----		-----		-----	-
TrMDHb7	:	-----		-----		-----	-
TrMDHb8	:	-----		-----		-----	-
TrMDHb9	:	-----		-----		-----	-
TrMDHb10	:	-----		-----		-----	-
TrMDHb11	:	-----		-----		-----	-
TrMDHb12	:	-----		-----		-----	-
TrMDHb13	:	-----		-----		-----	-
TrMDHb14	:	-----		-----		-----	-
TrMDHb15	:	-----		-----		-----	-
TrMDHb16	:	-----		-----		-----	-
TrMDHb17	:	-----		-----		-----	-
TrMDHb18	:	-----		-----		-----	-
TrMDHb19	:	-----		-----		-----	-
TrMDHb20	:	-----		-----		-----	-
TrMDHb21	:	-----		-----		-----	-
TrMDHb22	:	-----		-----		-----	-
TrMDHb23	:	-----		-----		-----	-
TrMDHb24	:	-----		-----		-----	-
TrMDHb25	:	TGGTTGAATGGAGAATTCATATCTACCGTTCAACAACGTGGTGCTG		-----		-----	-
TrMDHb26	:	-----		-----		-----	752
TrMDHb27	:	-----		-----		-----	-
TrMDHb28	:	-----		-----		-----	-
TrMDHb29	:	-----		-----		-----	-
TrMDHb30	:	TGGTTGAATGGAGAATTCATATCTACCGTTCAACAACGTGGTGCTGCAATTATTAAGGCT		-----		-----	582
TrMDHb31	:	TGGTTGAATGGAGAATTCATATCTACCGTTCAACAACGTGGTGCTGCAATTATTAAGGCT		-----		-----	424
TrMDHb32	:	TGGTTGAATGGAGAATTCATATCTACCGTTCAACAACGTGGTGCTGCAATTATTAAGGCT		-----		-----	424

	*	860	*	880	*	900
TrMDHb1	:	-----	:	-----	:	-----
TrMDHb2	:	-----	:	-----	:	-----
TrMDHb3	:	-----	:	-----	:	-----
TrMDHb4	:	-----	:	-----	:	-----
TrMDHb5	:	-----	:	-----	:	-----
TrMDHb6	:	-----	:	-----	:	-----
TrMDHb7	:	-----	:	-----	:	-----
TrMDHb8	:	-----	:	-----	:	-----
TrMDHb9	:	-----	:	-----	:	-----
TrMDHb10	:	-----	:	-----	:	-----
TrMDHb11	:	-----	:	-----	:	-----
TrMDHb12	:	-----	:	-----	:	-----
TrMDHb13	:	-----	:	-----	:	-----
TrMDHb14	:	-----	:	-----	:	-----
TrMDHb15	:	-----	:	-----	:	-----
TrMDHb16	:	-----	:	-----	:	-----
TrMDHb17	:	-----	:	-----	:	-----
TrMDHb18	:	-----	:	-----	:	-----
TrMDHb19	:	-----	:	-----	:	-----
TrMDHb20	:	-----	:	-----	:	-----
TrMDHb21	:	-----	:	-----	:	-----
TrMDHb22	:	-----	:	-----	:	-----
TrMDHb23	:	-----	:	-----	:	-----
TrMDHb24	:	-----	:	-----	:	-----
TrMDHb25	:	-----	:	-----	:	-----
TrMDHb26	:	-----	:	-----	:	-----
TrMDHb27	:	-----	:	-----	:	-----
TrMDHb28	:	-----	:	-----	:	-----
TrMDHb29	:	-----	:	-----	:	-----
TrMDHb30	:	AGAAAGCTTTCAAGTGG	:	-----	:	-----
TrMDHb31	:	AGAAAGCTTTCAAGCGCACTATCCGCTGCTAGCGCTGCTTGCGACCA	:	-----	:	-----
TrMDHb32	:	AGAAAGCTTTCAAGCGCACTATCCGCTGCTAGCGCTGCTTGCGACCA	:	-----	:	-----

	*	920	*	940	*	960	
TrMDHb1	:	-----	:	-----	:	-----	-
TrMDHb2	:	-----	:	-----	:	-----	-
TrMDHb3	:	-----	:	-----	:	-----	-
TrMDHb4	:	-----	:	-----	:	-----	-
TrMDHb5	:	-----	:	-----	:	-----	-
TrMDHb6	:	-----	:	-----	:	-----	-
TrMDHb7	:	-----	:	-----	:	-----	-
TrMDHb8	:	-----	:	-----	:	-----	-
TrMDHb9	:	-----	:	-----	:	-----	-
TrMDHb10	:	-----	:	-----	:	-----	-
TrMDHb11	:	-----	:	-----	:	-----	-
TrMDHb12	:	-----	:	-----	:	-----	-
TrMDHb13	:	-----	:	-----	:	-----	-
TrMDHb14	:	-----	:	-----	:	-----	-
TrMDHb15	:	-----	:	-----	:	-----	-
TrMDHb16	:	-----	:	-----	:	-----	-
TrMDHb17	:	-----	:	-----	:	-----	-
TrMDHb18	:	-----	:	-----	:	-----	-
TrMDHb19	:	-----	:	-----	:	-----	-
TrMDHb20	:	-----	:	-----	:	-----	-
TrMDHb21	:	-----	:	-----	:	-----	-
TrMDHb22	:	-----	:	-----	:	-----	-
TrMDHb23	:	-----	:	-----	:	-----	-
TrMDHb24	:	-----	:	-----	:	-----	-
TrMDHb25	:	-----	:	-----	:	-----	-
TrMDHb26	:	-----	:	-----	:	-----	-
TrMDHb27	:	-----	:	-----	:	-----	-
TrMDHb28	:	-----	:	-----	:	-----	-
TrMDHb29	:	-----	:	-----	:	-----	-
TrMDHb30	:	-----	:	-----	:	-----	-
TrMDHb31	:	GTTCTTGGAACCCCCAGGGCACCTTCGTTTCAATGGGAGTGTATTCTGATGGTTCTTAC				:	544
TrMDHb32	:	GTTCTTGGAACCCCCAGGGCACCTTCGTTTCAATGGGAGTGTATTCTGATGGTTCTTAC				:	544

	*	980	*	1000	*	1020	
TrMDHb1	:	-----	:	-----	:	-----	:
TrMDHb2	:	-----	:	-----	:	-----	:
TrMDHb3	:	-----	:	-----	:	-----	:
TrMDHb4	:	-----	:	-----	:	-----	:
TrMDHb5	:	-----	:	-----	:	-----	:
TrMDHb6	:	-----	:	-----	:	-----	:
TrMDHb7	:	-----	:	-----	:	-----	:
TrMDHb8	:	-----	:	-----	:	-----	:
TrMDHb9	:	-----	:	-----	:	-----	:
TrMDHb10	:	-----	:	-----	:	-----	:
TrMDHb11	:	-----	:	-----	:	-----	:
TrMDHb12	:	-----	:	-----	:	-----	:
TrMDHb13	:	-----	:	-----	:	-----	:
TrMDHb14	:	-----	:	-----	:	-----	:
TrMDHb15	:	-----	:	-----	:	-----	:
TrMDHb16	:	-----	:	-----	:	-----	:
TrMDHb17	:	-----	:	-----	:	-----	:
TrMDHb18	:	-----	:	-----	:	-----	:
TrMDHb19	:	-----	:	-----	:	-----	:
TrMDHb20	:	-----	:	-----	:	-----	:
TrMDHb21	:	-----	:	-----	:	-----	:
TrMDHb22	:	-----	:	-----	:	-----	:
TrMDHb23	:	-----	:	-----	:	-----	:
TrMDHb24	:	-----	:	-----	:	-----	:
TrMDHb25	:	-----	:	-----	:	-----	:
TrMDHb26	:	-----	:	-----	:	-----	:
TrMDHb27	:	-----	:	-----	:	-----	:
TrMDHb28	:	-----	:	-----	:	-----	:
TrMDHb29	:	-----	:	-----	:	-----	:
TrMDHb30	:	-----	:	-----	:	-----	:
TrMDHb31	:	AACGTACCAGCTGGACTCATCTATTTCATTCCCTGTCACCACTGCTAATGGGGAATGGAA-				:	603
TrMDHb32	:	AACGTACCAGCTGGACTCATCTATTTCATTCCCTGTCACCACTGCTAATGGGGAATGGAAA				:	604

	*	1040	*	1060	*	1080	
TrMDHb1	:	-----	:	-----	:	-----	:
TrMDHb2	:	-----	:	-----	:	-----	:
TrMDHb3	:	-----	:	-----	:	-----	:
TrMDHb4	:	-----	:	-----	:	-----	:
TrMDHb5	:	-----	:	-----	:	-----	:
TrMDHb6	:	-----	:	-----	:	-----	:
TrMDHb7	:	-----	:	-----	:	-----	:
TrMDHb8	:	-----	:	-----	:	-----	:
TrMDHb9	:	-----	:	-----	:	-----	:
TrMDHb10	:	-----	:	-----	:	-----	:
TrMDHb11	:	-----	:	-----	:	-----	:
TrMDHb12	:	-----	:	-----	:	-----	:
TrMDHb13	:	-----	:	-----	:	-----	:
TrMDHb14	:	-----	:	-----	:	-----	:
TrMDHb15	:	-----	:	-----	:	-----	:
TrMDHb16	:	-----	:	-----	:	-----	:
TrMDHb17	:	-----	:	-----	:	-----	:
TrMDHb18	:	-----	:	-----	:	-----	:
TrMDHb19	:	-----	:	-----	:	-----	:
TrMDHb20	:	-----	:	-----	:	-----	:
TrMDHb21	:	-----	:	-----	:	-----	:
TrMDHb22	:	-----	:	-----	:	-----	:
TrMDHb23	:	-----	:	-----	:	-----	:
TrMDHb24	:	-----	:	-----	:	-----	:
TrMDHb25	:	-----	:	-----	:	-----	:
TrMDHb26	:	-----	:	-----	:	-----	:
TrMDHb27	:	-----	:	-----	:	-----	:
TrMDHb28	:	-----	:	-----	:	-----	:
TrMDHb29	:	-----	:	-----	:	-----	:
TrMDHb30	:	-----	:	-----	:	-----	:
TrMDHb31	:	-----	:	-----	:	-----	:
TrMDHb32	:	ATTGTTCAAGGACTTTCAATTGACGAGTTCTCAAGGAAGAAGTTGGACTTGACAGCTGAA					:

* 1100 *

TrMDHb1 : ----- : -
TrMDHb2 : ----- : -
TrMDHb3 : ----- : -
TrMDHb4 : ----- : -
TrMDHb5 : ----- : -
TrMDHb6 : ----- : -
TrMDHb7 : ----- : -
TrMDHb8 : ----- : -
TrMDHb9 : ----- : -
TrMDHb10 : ----- : -
TrMDHb11 : ----- : -
TrMDHb12 : ----- : -
TrMDHb13 : ----- : -
TrMDHb14 : ----- : -
TrMDHb15 : ----- : -
TrMDHb16 : ----- : -
TrMDHb17 : ----- : -
TrMDHb18 : ----- : -
TrMDHb19 : ----- : -
TrMDHb20 : ----- : -
TrMDHb21 : ----- : -
TrMDHb22 : ----- : -
TrMDHb23 : ----- : -
TrMDHb24 : ----- : -
TrMDHb25 : ----- : -
TrMDHb26 : ----- : -
TrMDHb27 : ----- : -
TrMDHb28 : ----- : -
TrMDHb29 : ----- : -
TrMDHb30 : ----- : -
TrMDHb31 : ----- : -
TrMDHb32 : GAGTTATCCGAGGAAAAGAGTTTGGCATACT : 695

Figure 61 Consensus contig nucleotide sequence of TrMDHc

```

      *           20           *           40           *           60
TrMDHc : AAAGNGAATTGGAATATACGACACTCCATTCCATACTTCCATTCCNTACTTTGCTTTCTC : 60

      *           80           *           100          *           120
TrMDHc : GCTCTCTCTCTCTTTATTCTCGAAAAGCTTTTTCAGCCAACAACGGAGAGAATTATGAGG : 120

      *           140          *           160           *           180
TrMDHc : CCGTCGATGCTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGC : 180

      *           200          *           220           *           240
TrMDHc : CGTGGCTATGCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGC : 240

      *           260          *           280           *           300
TrMDHc : GGGATCGGCCAGCCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCT : 300

      *           320          *           340           *           360
TrMDHc : CTTTATGATATTGCTGGAACCCCTGGTGTGCGCGCTGATGTCAGCCACATCAACTCCAGA : 360

      *           380          *           400           *           420
TrMDHc : TCTGAGGTAAC TGGGTATGCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGAT : 420

      *           440          *           460           *           480
TrMDHc : GTTGTATAATTCTCTGCTGGTGTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTC : 480

      *           500          *           520           *           540
TrMDHc : AATATTAACGCTGGCATTGTCAAGTCACTTGCCACTGCTATTTCTAAGTACTGCCCCCAT : 540

      *           560          *           580           *           600
TrMDHc : GCCCTTGTTAACATGATAAGCAACCCTGTGAACTCCACCGTTCCCATTGCTGCAGAGGTT : 600

      *           620          *           640           *           660
TrMDHc : TTCAAGAAGGCAGGGACATATGACGAGAAGAGATTGTTTGGGGTTACAACCCCTTGATGTA : 660

      *           680          *           700           *           720
TrMDHc : GTCAGGGCAAAAAC TTTCTATGCCGGGAAAGCTAAAGTTCCAGTTGCCGAGGTCAATGTA : 720

      *           740          *           760           *           780
TrMDHc : CCTGTTATAGGAGGCCATGCAGGAGTTACTATTCTTCCATTATTTTNTCAGGCAACACCT : 780

      *           800          *           820           *           840
TrMDHc : CAAGCCAATCTGGGTGATGATAACCTTAAGGNTTTAACGGNANGGACACAAGATGGAGGA : 840

      *           860          *           880           *           900
TrMDHc : ACAGAAGTTGNGACCGCCAAGGCTGGAAAGGGTTCTGCAACTTTGTCAATGGCTTATGCT : 900

      *           920          *           940           *           960
TrMDHc : GGAGCCATATTTGCTGATGCTNGCCTCAAAGGNCTGAATGGAGTTCCAGATGTTATTGAG : 960

```

* 980 * 1000 * 1020
 TrMDHc : TGCTCATATGTGCAATCCAATATCATCTCTGACCTTCCTTTCTTTGCTTCCAAGGTGAGG : 1020

* 1040 * 1060 * 1080
 TrMDHc : ATTGGGAAGAATGGTGTGGAAGAAATTCTGGGCTTAGGTTCTCTCACAGATTTCGAGCAA : 1080

* 1100 * 1120 * 1140
 TrMDHc : CAAGGCCTTGAAAACCTCAAGGCTGAACTCAAATCATCTATTGAAAAGGGAATCAAATTT : 1140

* 1160 * 1180 * 1200
 TrMDHc : GCCTCCCAGTAATCGAACATGTCATACATTACTGGATTTTCCATTTAGAACCAGATCAA : 1200

* 1220 * 1240 * 1260
 TrMDHc : ATTTTGCAAATTCAGAACAAATTGTTTGTAATGTTGCCGGTAGGTATACCCCTAGATTTAA : 1260

* 1280 * 1300 * 1320
 TrMDHc : TAAGTAAATCTGCGAGAGCAGTTTATTGCTGCAGGGACTGAAATTAAAACCAGTTTTAGG : 1320

* 1340 * 1360 * 1380
 TrMDHc : TTGGCCTTTCCATTTCGTAATGGCCCTTCATTGTTGCATGNTTTCATATAATGCAATTGAA : 1380

* 1400
 TrMDHc : GGGTGNTGGNCANCGATACACANCCCCC : 1408

Figure 62 Deduced amino acid sequence of TrMDHc

TrMDHc : MRPSMLRSVQSAVSRASSHLTRRGYATEPVPERKVAILGAAGGIGQPLSLLMKLNPLVST : 60

TrMDHc : LSLYDIAGTPGVAADVSHINSRSEVTGYAGEEELGKALEGADVVIIPAGVPRKPGMTRDD : 120

TrMDHc : LFNINAGIVKSLATAISKYCPHALVMISNPFVNSTVPPIAAEVFKKAGTYDEKRLFGVTTL : 180

TrMDHc : DVVRAKTFYAGKAKVPVAEVNVPVIGGHAGVTILPLFXQATPQANLGDDTLKXLTXXTQD : 240

TrMDHc : GGTEVXTAKAGKGSATLSMAYAGAI FADAXLKXLNGVPDVIECSYVQSNIISDLPFFASK : 300

TrMDHc : VRIGKNGVEEILGLGSLTDFEQQLENLKAELKSSIEKGIKFASQ : 345

Figure 63 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHc

	*	20	*	40	*	60	
TrMDHc1 :		AAAGNGAATTGGAATNT	CGAC	CTCCATTCCNTACT	TTATTTCATTCATCGCT	TCTCTCTCT	: 60
TrMDHc2 :		GTGATATTGGAATATAC	NGCACTCCATTCCATACT	TTATTTCATTCATCGCT	TCTCTCTCT	TCT	: 59
TrMDHc3 :		-----	GNNCATCGA	CACCTGGCTTCCCTACCT	TCTTT	NTTTATCGCT	: 42
TrMDHc4 :		-----	-----	CNACT	CCATTCCNTACTTTT	NTTNTTNTCC	: 30
TrMDHc5 :		-----	-----	CCATCC	TTCCNTACTTT	NTTCTCGCT	: 27
TrMDHc6 :		-----	-----	CNTCCAT	CCNTACTTT	NTTCTCGCT	: 27
TrMDHc7 :		-----	-----	CNTTCC	TTCCCTACTTT	CATTCCATCG	: 27
TrMDHc8 :		-----	-----	TCCCAT	TTCCNTACTTT	NTTNTTNTCC	: 27
TrMDHc9 :		-----	-----	TCCATT	CCNTACTCT	ATTTNTCGCT	: 25
TrMDHc10 :		-----	-----	TCC	TTCCATACTTT	ATTTCATCGCT	: 25
TrMDHc11 :		-----	-----	-----	-----	-----	: -
TrMDHc12 :		-----	-----	-----	-----	-----	: -
TrMDHc13 :		-----	-----	-----	-----	-----	: -
TrMDHc14 :		-----	-----	-----	-----	-----	: -
TrMDHc15 :		-----	-----	-----	-----	-----	: -
TrMDHc16 :		-----	-----	-----	-----	-----	: -
TrMDHc17 :		-----	-----	-----	-----	-----	: -

	*	80	*	100	*	120	
TrMDHc1 :		CTCTCTCTCTTTATTCTCGAAAAGCTTT	TTCAGCCAACAACG	AGAGAAT	AATGAGGCCGTCG		: 122
TrMDHc2 :		CTCTCTCTCT-T-TATTCTCGAAAAGCTTTT	TTCAGCCAACAACG	AGAGAAT	AATGAGGCCGTCG		: 119
TrMDHc3 :		CTCTCTCTCTTTTATTCTCGAAAAGCTTTT	TTCAGCCAACAACGAGAGAATTATGAGGCCGTCG			: 105	
TrMDHc4 :		CTCTCTCTCTCTTATTCTCGAAAAGCTTTT	TTCAGCCAACAACGAGAGAATTATGAGGCCGTCG			: 91	
TrMDHc5 :		CTCTCTCTCT-TTTATTCTCGAAAAGCTTTT	TTCAGCCAACAACGAGAGAATTATGAGGCCGTCG			: 88	
TrMDHc6 :		CTCTCTCTCT-TTTATTCTCGAAAAGCTTTT	TTCAGCCAACAACGAGAGAATTATGAGGCCGTCG			: 87	
TrMDHc7 :		CTCTCTCTCTTTTATTCTCGAAAAGCTTTT	TTCAGCCAACAACGAGAGAATTATGAGGCCGTCG			: 90	
TrMDHc8 :		CTCTCTCTCTTTTATTCTCGAAAAGCTTTT	TTCAGCCAACAACGAGAGAATTATGAGGCCGTCG			: 89	
TrMDHc9 :		CTCTCTCTCTTTTATTCTCGAAAAGCTTTT	TTCAGCCAACAACGAGAGAATTATGAGGCCGTCG			: 87	
TrMDHc10 :		CTCTCTCTCT-TTTATTCTCGAAAAGCTTTT	TTCAGCCAACAACGAGAGAATTATGAGGCCGTCG			: 86	
TrMDHc11 :		-----	GNNCTCTCG-AAAGCTTTT	NGCC	TAACGGAGAGAATTATGAGGCCGTCG		: 48
TrMDHc12 :		-----	TTCTCGAAAAGCTTTT	AGCC-ACAACG-AGAGAA	AATGAGGCCGTCG		: 46
TrMDHc13 :		-----	TTCTCG-AAAGCTTTT	TTCAGCC-ACAACG	TAAGAGAATTATGAGGCCGTCG		: 48
TrMDHc14 :		-----	-----	-----	-----		: -
TrMDHc15 :		-----	-----	-----	-----		: -
TrMDHc16 :		-----	-----	-----	-----		: -
TrMDHc17 :		-----	-----	-----	-----		: -

	*	140	*	160	*	180	
TrMDHc1 :		ATGCTCAGATCCGTCCAATCAGCCGT	TCCCGCGCCTCTCTCACCT	AACCCGCCGTGGCTAT			: 185
TrMDHc2 :		ATGCTCAGATCCGTCCAATCAGCCGT	TCCCGCGCCTCTCTCACCT	AACCCGCCGTGGCTAT			: 182
TrMDHc3 :		ATGCTCAGATCCGTCCAATCAGCCGT	TCCCGCGCCTCTCTCACCT	AACCCGCCGTGGCTAT			: 168
TrMDHc4 :		ATGCTCAGATCTGTCCAATCAGCCGT	TCCCGCGCCTCTCTCACCT	AACCCGCCGTGGCTAT			: 154
TrMDHc5 :		ATGCTCAGATCCGTCCAATCAGCCGT	TCCCGCGCCTCTCTCACCT	AACCCGCCGTGGCTAT			: 151
TrMDHc6 :		ATGCTCAGATCCGTCCAATCAGCCGT	TCCCGCGCCTCTCTCACCT	AACCCGCCGTGGCTAT			: 150
TrMDHc7 :		ATGCTCAGATCCGTCCAATCAGCCGT	TCCCGCGCCTCTCTCACCT	AACCCGCCGTGGCTAT			: 153
TrMDHc8 :		ATGCTCAGATCCGTCCAATCAGCCGT	TCCCGCGCCTCTCTCACCT	AACCCGCCGTGGCTAT			: 152
TrMDHc9 :		ATGCTCAGATCCGTCCAATCAGCCGT	TCCCGCGCCTCTCTCACCT	AACCCGCCGTGGCTAT			: 150
TrMDHc10 :		ATGCTCAGATCCGTCCAATCAGCCGT	TCCCGCGCCTCTCTCACCT	AACCCGCCGTGGCTAT			: 149
TrMDHc11 :		ATGCTCAGATCCGTCCAATCAGCCGT	TCCCGCGCCTCTCTCACCT	AACCCGCCGTGGCTAT			: 111
TrMDHc12 :		ATGCTCAGATCTGTCC-ATCAGCCGT	TCCCGCGCCTCTCTCACCT	AACCCGCCGTGGCTAT			: 108
TrMDHc13 :		ATGCTCAGATCTGTCCAATCAGCCGT	TCCCGCGCCTCTCTCACCT	AACCCGCCGTGGCTAT			: 111
TrMDHc14 :		-----	-----	-----	-----		: -
TrMDHc15 :		-----	-----	-----	-----		: -
TrMDHc16 :		-----	-----	-----	-----		: -
TrMDHc17 :		-----	-----	-----	-----		: -

	*	200	*	220	*	240	*	
TrMDHc1	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCGCGCGGGATCGG		A		CAG : 248
TrMDHc2	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCGCGCGGGATCGG		A		CAG : 245
TrMDHc3	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCGCGCGGGATCGG		A		CAG : 231
TrMDHc4	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCGCGCGGGATCGG		A		CAG : 217
TrMDHc5	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCGCGCGGGATCGG		A		CAG : 214
TrMDHc6	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCGCGCGGGATCGG		A		CAG : 213
TrMDHc7	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCGCGCGGGATCGG		A		CAG : 216
TrMDHc8	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCGCGCGGGATCGG		A		CAG : 215
TrMDHc9	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCGCGCGGGATCGG		A		CAG : 213
TrMDHc10	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCGCGCGGGATCGG		A		CAG : 212
TrMDHc11	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCGCGCGGGATCGG		A		CAG : 174
TrMDHc12	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCGCGCGGGATCGG		A		CAG : 171
TrMDHc13	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCGCGCGGGATCGG		A		CAG : 174
TrMDHc14	:	-----						-
TrMDHc15	:	-----						-
TrMDHc16	:	-----						-
TrMDHc17	:	-----						-

		260	*	280	*	300	*	
TrMDHc1	:	CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT						: 311
TrMDHc2	:	CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT						: 308
TrMDHc3	:	CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT						: 294
TrMDHc4	:	CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT						: 280
TrMDHc5	:	CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT						: 277
TrMDHc6	:	CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT						: 276
TrMDHc7	:	CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT						: 279
TrMDHc8	:	CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT						: 278
TrMDHc9	:	CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT						: 276
TrMDHc10	:	CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT						: 275
TrMDHc11	:	CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT						: 237
TrMDHc12	:	CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT						: 234
TrMDHc13	:	CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT						: 237
TrMDHc14	:	-----						-
TrMDHc15	:	-----						-
TrMDHc16	:	-----						-
TrMDHc17	:	-----						-

		320	*	340	*	360	*	3	
TrMDHc1	:	GGAACCCCTGGTGTGCGCGCTGATGTGAGCCACATCAACTCCAGATCTGAGGTAAC							: 374
TrMDHc2	:	GGAACCCCTGGTGTGCGCGCTGATGTGAGCCACATCAACTCCAGATCTGAGGTAAC							: 371
TrMDHc3	:	GGAACCCCTGGTGTGCGCGCTGATGTGAGCCACATCAACTCCAGATCTGAGGTAAC							: 357
TrMDHc4	:	GGAACCCCTGGTGTGCGCGCTGATGTGAGCCACATCAACTCCAGATCTGAGGTAAC							: 343
TrMDHc5	:	GGAACCCCTGGTGTGCGCGCTGATGTGAGCCACATCAACTCCAGATCTGAGGTAAC							: 340
TrMDHc6	:	GGAACCCCTGGTGTGCGCGCTGATGTGAGCCACATCAACTCCAGATCTGAGGTAAC							: 339
TrMDHc7	:	GGAACCCCTGGTGTGCGCGCTGATGTGAGCCACATCAACTCCAGATCTGAGGTAAC							: 342
TrMDHc8	:	GGAACCCCTGGTGTGCGCGCTGATGTGAGCCACATCAACTCCAGATCTGAGGTAAC							: 341
TrMDHc9	:	GGAACCCCTGGTGTGCGCGCTGATGTGAGCCACATCAACTCCAGATCTGAGGTAAC							: 339
TrMDHc10	:	GGAACCCCTGGTGTGCGCGCTGATGTGAGCCACATCAACTCCAGATCTGAGGTAAC							: 338
TrMDHc11	:	GGAACCCCTGGTGTGCGCGCTGATGTGAGCCACATCAACTCCAGATCTGAGGTAAC							: 300
TrMDHc12	:	GGAACCCCTGGTGTGCGCGCTGATGTGAGCCACATCAACTCCAGATCTGAGGTAAC							: 297
TrMDHc13	:	GGAACCCCTGGTGTGCGCGCTGATGTGAGCCACATCAACTCCAGATCTGAGGTAAC							: 300
TrMDHc14	:	-----GNGTGTGCGCGCTGNGTGTGAGCCACATCAACTCCAGATCTGAGGTAAC							: 54
TrMDHc15	:	-----GNGTGTGT-NGCC-CAT-AACTCC-GATCTGAGGTAAC							: 41
TrMDHc16	:	-----							-
TrMDHc17	:	-----							-

	80	*	400	*	420	*	440	
TrMDHc1 :	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT							: 437
TrMDHc2 :	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT							: 434
TrMDHc3 :	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT							: 420
TrMDHc4 :	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT							: 406
TrMDHc5 :	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT							: 403
TrMDHc6 :	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT							: 402
TrMDHc7 :	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT							: 405
TrMDHc8 :	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT							: 404
TrMDHc9 :	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT							: 402
TrMDHc10 :	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT							: 401
TrMDHc11 :	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT							: 363
TrMDHc12 :	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT							: 360
TrMDHc13 :	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT							: 363
TrMDHc14 :	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT							: 117
TrMDHc15 :	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT							: 104
TrMDHc16 :	-----							: -
TrMDHc17 :	-----							: -

	*	460	*	480	*	500	
TrMDHc1 :	GTGCCCAGAAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAA					CGCTGGCATTGTCAAG	: 500
TrMDHc2 :	GTGCCCAGAAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAA					CGCTGGCATTGTCAAG	: 497
TrMDHc3 :	GTGCCCAGAAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAA					CGCTGGCATTGTCAAG	: 483
TrMDHc4 :	GTGCCCAGAAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAA					CGCTGGCATTGTCAAG	: 469
TrMDHc5 :	GTGCCCAGAAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAA					CGCTGGCATTGTCAAG	: 466
TrMDHc6 :	GTGCCCAGAAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAA					CGCTGGCATTGTCAAG	: 465
TrMDHc7 :	GTGCCCAGAAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAA					CGCTGGCATTGTCAAG	: 468
TrMDHc8 :	GTGCCCAGAAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAA					CGCTGGCATTGTCAAG	: 467
TrMDHc9 :	GTGCCCAGAAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAA					CGCTGGCATTGTCAAG	: 465
TrMDHc10 :	GTGCCCAGAAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAA					CGCTGGCATTGTCAAG	: 464
TrMDHc11 :	GTGCCCAGAAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAA					CGCTGGCATTGTCAAG	: 426
TrMDHc12 :	GTGCCCAGAAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAA					CGCTGGCATTGTCAAG	: 423
TrMDHc13 :	GTGCCCAGAAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAA					CGCTGGCATTGTCAAG	: 426
TrMDHc14 :	GTGCCCAGAAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAA					CGCTGGCATTGTCAAG	: 180
TrMDHc15 :	GTGCCCAGAAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAA					CGCTGGCATTGTCAAG	: 167
TrMDHc16 :	-----						: -
TrMDHc17 :	-----						: -

	*	520	*	540	*	560	
TrMDHc1 :	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATG					-----	: 537
TrMDHc2 :	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT						: 560
TrMDHc3 :	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT						: 546
TrMDHc4 :	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT						: 532
TrMDHc5 :	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT						: 529
TrMDHc6 :	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT						: 528
TrMDHc7 :	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT						: 531
TrMDHc8 :	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT						: 530
TrMDHc9 :	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT						: 528
TrMDHc10 :	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT						: 527
TrMDHc11 :	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT						: 489
TrMDHc12 :	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT						: 486
TrMDHc13 :	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT						: 489
TrMDHc14 :	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT						: 243
TrMDHc15 :	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT						: 230
TrMDHc16 :	-----					TTG	: 3
TrMDHc17 :	-----						: -

	580	600	620	
TrMDHc1	-----			-
TrMDHc2	GTGAACTCCACCGTTCCCATTTGCTGCAGAGGTTTTCAAGAAGGCAGGG			608
TrMDHc3	GTGAACTCCACCGTTCCCATTTGCTGCAGG-----			575
TrMDHc4	GTGAACTCCACCGTTCCCATTTGCTGCAGAGG-----			563
TrMDHc5	GTGAACTCCACCGTTCCCATTTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATAT-----			583
TrMDHc6	GTGAACTCCACCGTTCCCATTTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG			591
TrMDHc7	GTGAACTCCACCGTTCCCATTTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG			594
TrMDHc8	GTGAACTCCACCGTTCCCATTTGCTGC-----			556
TrMDHc9	GTGAACTCCACCGTTCCCATTTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG			591
TrMDHc10	GTGAACTCCACCGTTCCCATTTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG			590
TrMDHc11	GTGAACTCCACCGTTCCCATTTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG			552
TrMDHc12	GTGAACTCCACCGTTCCCATTTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG			549
TrMDHc13	GTGAACTCCACCGTTCCCATTTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG			552
TrMDHc14	GTGAACTCCACCGTTCCCATTTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG			306
TrMDHc15	GTGAACTCCACCGTTCCCATTTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG			293
TrMDHc16	-----			-
TrMDHc17	-----			-

	640	660	680	
TrMDHc1	-----			-
TrMDHc2	-----			-
TrMDHc3	-----			-
TrMDHc4	-----			-
TrMDHc5	-----			-
TrMDHc6	AGATTGT-----			598
TrMDHc7	AGATTGTTTGGGGTTACAACCCTTGATGTAGTCAGGGCGAAAACCTTTTATGCCGGGAAAGCT			657
TrMDHc8	-----			-
TrMDHc9	AGATTGTTTGGGGTTACAACCCTTGATGTAGTCAGGGCGAAAACCTTTCTATGCCGGGAAAGCT			654
TrMDHc10	AGATTGTTTGGGGTTACAACCCTTGATGTAGTCAGGGCGAAAACCTTTTATGCCGGGAAAGCT			652
TrMDHc11	AGATTGTTTGGGGTTACAACCCTTG-----			577
TrMDHc12	AGATTGTTTGGGGTTACAACCCTTGATGTAGTCAGGGCAAAAACCT-----			594
TrMDHc13	AGATTGTTTGGGGTTACAACCCTTGATGTAGTCAGGGCAAAAACCTTTTATGCCGGGAAAGCT			615
TrMDHc14	AGATTGTTTGGGGTTACAACCCTTGATGTAGTCAGGGCAAAAACCTTTCTATGCCGGGAAAGCT			369
TrMDHc15	AGATTGTTTGGGGTTACAACCCTTGATGTAGTCAGGGCAAAAACCTTTCTATGCCGGGAAAGCT			356
TrMDHc16	-----			-
TrMDHc17	-----			-

	700	720	740	
TrMDHc1	-----			-
TrMDHc2	-----			-
TrMDHc3	-----			-
TrMDHc4	-----			-
TrMDHc5	-----			-
TrMDHc6	-----			-
TrMDHc7	AAAGTTCCAGTTGCCGAGGTCAATGTACCTGTTTGGAGGCCATGCAGGAGTTACTATTNTT			720
TrMDHc8	-----			-
TrMDHc9	AAAGTTCCAGTTGCCGAGGTCAATGTAC-----			682
TrMDHc10	AAAGTTCCAGTTGCCGAGGTCAATGTACCTGTTTGGAGGCC-TGG-NGAG-TNCTATT-TT			711
TrMDHc11	-----			-
TrMDHc12	-----			-
TrMDHc13	AAAGTTCCAGTTGCCGAGGTCAATGTACCTGTTATAGGAGGCCATGCAGGAGTTACTATTCT			678
TrMDHc14	AAAGTTCCAGTTGCCGAGGTCAATGTACCTGTTATAGGAGGCCATGCAGGAGTTACTATTCT			432
TrMDHc15	AAAGTTCCAGTTGCCGAGGTCAATGTACCTGTTATAGGAGGCCATGCAGGAGTTACTATTCT			419
TrMDHc16	-----			-
TrMDHc17	-----			-

	760	*	780	*	800	*	82
TrMDHc1 :	-----						-
TrMDHc2 :	-----						-
TrMDHc3 :	-----						-
TrMDHc4 :	-----						-
TrMDHc5 :	-----						-
TrMDHc6 :	-----						-
TrMDHc7 :	CCATTATTTTNTAAGG	-	AACACCTNAAGCCAATNTGGNTGATGAAACCTTNAGGNTTTAACG				782
TrMDHc8 :	-----						-
TrMDHc9 :	-----						-
TrMDHc10 :	CCGTTTITTTTITTAGG	-	GANNCT	-	NANCCANT	-	769
TrMDHc11 :	-----						-
TrMDHc12 :	-----						-
TrMDHc13 :	CCATTATTTTNTNAGGCAACACCTNAAGCCAATNTGGGTGANGATNCCCTTAAGGNTTTAACG						741
TrMDHc14 :	CCATTATTTTCTCAGGCAACACCTCAAGCCAATCTGGATGATGATACCATTAAGGCTCTAACG						495
TrMDHc15 :	CCATTATTTTCTCAGGCAACACCTCAAGCCAATCTGGATGATGATACCATTAAGGCTCTAACG						482
TrMDHc16 :	-----						-
TrMDHc17 :	-----						-

	0	*	840	*	860	*	880
TrMDHc1 :	-----						-
TrMDHc2 :	-----						-
TrMDHc3 :	-----						-
TrMDHc4 :	-----						-
TrMDHc5 :	-----						-
TrMDHc6 :	-----						-
TrMDHc7 :	GNANGGECNCAAGATGGCGGAACNGAA	-	TTGNGACCGCCAAGGCTT				827
TrMDHc8 :	-----						-
TrMDHc9 :	-----						-
TrMDHc10 :	GG	-	NNGECNCAAZANG	-	GGGAACAAA	-	801
TrMDHc11 :	-----						-
TrMDHc12 :	-----						-
TrMDHc13 :	GNANGGACCAANANGGAGGAACA		NAANTTNGACC		CCANGG	-	801
TrMDHc14 :	GGAAGGACACAAGATGGAGGAACAGAAGTTGT		GACCGCCAAGGCTGGA		AAGGGTTNT	-	558
TrMDHc15 :	GGAAGGACACAAGATGGAGGAACAGAAGTTGT		GACCGCCAAGGCTGGA		AAGGGTTCTGCAACT		545
TrMDHc16 :	-----						-
TrMDHc17 :	-----						-

	*	900	*	920	*	940	
TrMDHc1 :	-----					-	
TrMDHc2 :	-----					-	
TrMDHc3 :	-----					-	
TrMDHc4 :	-----					-	
TrMDHc5 :	-----					-	
TrMDHc6 :	-----					-	
TrMDHc7 :	-----					-	
TrMDHc8 :	-----					-	
TrMDHc9 :	-----					-	
TrMDHc10 :	-----					-	
TrMDHc11 :	-----					-	
TrMDHc12 :	-----					-	
TrMDHc13 :	TT	-	NNAATGGN			811	
TrMDHc14 :	TTGTCAATGGCTTATGCTGGAGCCATATTTGCTGATGCT		GCCTCAAAGG		CTGAATGGAGTT	621	
TrMDHc15 :	TTGTCAATGGCT					557	
TrMDHc16 :	-----			CTGNTGCTNGCCT	-	NANGGNTGAATGGAGTT	34
TrMDHc17 :	-----					GNGNGTT	7

	*	960	*	980	*	1000	
TrMDHc1	:	-----	:	-----	:	-----	:
TrMDHc2	:	-----	:	-----	:	-----	:
TrMDHc3	:	-----	:	-----	:	-----	:
TrMDHc4	:	-----	:	-----	:	-----	:
TrMDHc5	:	-----	:	-----	:	-----	:
TrMDHc6	:	-----	:	-----	:	-----	:
TrMDHc7	:	-----	:	-----	:	-----	:
TrMDHc8	:	-----	:	-----	:	-----	:
TrMDHc9	:	-----	:	-----	:	-----	:
TrMDHc10	:	-----	:	-----	:	-----	:
TrMDHc11	:	-----	:	-----	:	-----	:
TrMDHc12	:	-----	:	-----	:	-----	:
TrMDHc13	:	-----	:	-----	:	-----	:
TrMDHc14	:	CCAGATGTTATTGAGTGCTCATATGTGCAATCCAATATCATCTCTGACCTTCTTTCTTTGCT					: 684
TrMDHc15	:	-----					:
TrMDHc16	:	-CNGANGTTATTGAAGCTCTCATATGTGCAATCCAATATCATCTNTGACCTTCCTTTCTTTGCT					: 96
TrMDHc17	:	CCAGATGTTATTGAGTGCT-NTATGTGC-AT-CATAT-NTCTCTGACCTTCCTTTCTTTGCT					: 66

	*	1020	*	1040	*	1060	*	
TrMDHc1	:	-----	:	-----	:	-----	:	-
TrMDHc2	:	-----	:	-----	:	-----	:	-
TrMDHc3	:	-----	:	-----	:	-----	:	-
TrMDHc4	:	-----	:	-----	:	-----	:	-
TrMDHc5	:	-----	:	-----	:	-----	:	-
TrMDHc6	:	-----	:	-----	:	-----	:	-
TrMDHc7	:	-----	:	-----	:	-----	:	-
TrMDHc8	:	-----	:	-----	:	-----	:	-
TrMDHc9	:	-----	:	-----	:	-----	:	-
TrMDHc10	:	-----	:	-----	:	-----	:	-
TrMDHc11	:	-----	:	-----	:	-----	:	-
TrMDHc12	:	-----	:	-----	:	-----	:	-
TrMDHc13	:	-----	:	-----	:	-----	:	-
TrMDHc14	:	TCCAAGGTGAGGATTGGGAANAATGGTGTGGGAANAAT					:	722
TrMDHc15	:	-----					:	-
TrMDHc16	:	TCCAAGGNNNGGATTGGGAAGAATGGTGTGGGAAGATTCTG					:	138
TrMDHc17	:	TCC-AGGTGAGCATTGGGAAGAATGGTGTGGGAAGAAATTCTGGGCTTAGGTTCTCTCACAGAT					:	128

		1080	*	1100	*	1120	*	
TrMDHc1	:	-----	:	-----	:	-----	:	-
TrMDHc2	:	-----	:	-----	:	-----	:	-
TrMDHc3	:	-----	:	-----	:	-----	:	-
TrMDHc4	:	-----	:	-----	:	-----	:	-
TrMDHc5	:	-----	:	-----	:	-----	:	-
TrMDHc6	:	-----	:	-----	:	-----	:	-
TrMDHc7	:	-----	:	-----	:	-----	:	-
TrMDHc8	:	-----	:	-----	:	-----	:	-
TrMDHc9	:	-----	:	-----	:	-----	:	-
TrMDHc10	:	-----	:	-----	:	-----	:	-
TrMDHc11	:	-----	:	-----	:	-----	:	-
TrMDHc12	:	-----	:	-----	:	-----	:	-
TrMDHc13	:	-----	:	-----	:	-----	:	-
TrMDHc14	:	-----	:	-----	:	-----	:	-
TrMDHc15	:	-----	:	-----	:	-----	:	-
TrMDHc16	:	-----	:	-----	:	-----	:	-
TrMDHc17	:	TTCGAGCAACAAGGCCTTGAAAACCTCAAGGCTGAACTCAAATCATCTATTGAAAAGGGAATC					:	191

	1140	*	1160	*	1180	*	1	
TrMDHc1	:	-----						:
TrMDHc2	:	-----						:
TrMDHc3	:	-----						:
TrMDHc4	:	-----						:
TrMDHc5	:	-----						:
TrMDHc6	:	-----						:
TrMDHc7	:	-----						:
TrMDHc8	:	-----						:
TrMDHc9	:	-----						:
TrMDHc10	:	-----						:
TrMDHc11	:	-----						:
TrMDHc12	:	-----						:
TrMDHc13	:	-----						:
TrMDHc14	:	-----						:
TrMDHc15	:	-----						:
TrMDHc16	:	-----						:
TrMDHc17	:	AAATTTGCCTCCCAGTAATCGAACATGTCATACATTACTGGATTTTCCATTTAGAACCAGAT						: 254

	200	*	1220	*	1240	*	1260	
TrMDHc1	:	-----						:
TrMDHc2	:	-----						:
TrMDHc3	:	-----						:
TrMDHc4	:	-----						:
TrMDHc5	:	-----						:
TrMDHc6	:	-----						:
TrMDHc7	:	-----						:
TrMDHc8	:	-----						:
TrMDHc9	:	-----						:
TrMDHc10	:	-----						:
TrMDHc11	:	-----						:
TrMDHc12	:	-----						:
TrMDHc13	:	-----						:
TrMDHc14	:	-----						:
TrMDHc15	:	-----						:
TrMDHc16	:	-----						:
TrMDHc17	:	CAAATTTTGCAAATTCAGAACAAATTGTTTGTAATGTTGCCGGTAGGTATACCCCTAGATTAA						: 317

	*	1280	*	1300	*	1320	
TrMDHc1	:	-----					:
TrMDHc2	:	-----					:
TrMDHc3	:	-----					:
TrMDHc4	:	-----					:
TrMDHc5	:	-----					:
TrMDHc6	:	-----					:
TrMDHc7	:	-----					:
TrMDHc8	:	-----					:
TrMDHc9	:	-----					:
TrMDHc10	:	-----					:
TrMDHc11	:	-----					:
TrMDHc12	:	-----					:
TrMDHc13	:	-----					:
TrMDHc14	:	-----					:
TrMDHc15	:	-----					:
TrMDHc16	:	-----					:
TrMDHc17	:	TAAGTAAATCTGCGAGAGCAGTTTATTGCTGCAGGGACTGAAATTAAAACCAAGTTTATAGGTTG					: 380

	*	1340	*	1360	*	1380		
TrMDHc1	:	-----	:	-----	:	-----	:	
TrMDHc2	:	-----	:	-----	:	-----	:	
TrMDHc3	:	-----	:	-----	:	-----	:	
TrMDHc4	:	-----	:	-----	:	-----	:	
TrMDHc5	:	-----	:	-----	:	-----	:	
TrMDHc6	:	-----	:	-----	:	-----	:	
TrMDHc7	:	-----	:	-----	:	-----	:	
TrMDHc8	:	-----	:	-----	:	-----	:	
TrMDHc9	:	-----	:	-----	:	-----	:	
TrMDHc10	:	-----	:	-----	:	-----	:	
TrMDHc11	:	-----	:	-----	:	-----	:	
TrMDHc12	:	-----	:	-----	:	-----	:	
TrMDHc13	:	-----	:	-----	:	-----	:	
TrMDHc14	:	-----	:	-----	:	-----	:	
TrMDHc15	:	-----	:	-----	:	-----	:	
TrMDHc16	:	-----	:	-----	:	-----	:	
TrMDHc17	:	GCCTTCCATTTCGTAATGGCCCTTCATTGTTGCATGNTTTCATATAATGCAATTGAAGGGTGN					:	443

	*	1400	
TrMDHc1	:	-----	:
TrMDHc2	:	-----	:
TrMDHc3	:	-----	:
TrMDHc4	:	-----	:
TrMDHc5	:	-----	:
TrMDHc6	:	-----	:
TrMDHc7	:	-----	:
TrMDHc8	:	-----	:
TrMDHc9	:	-----	:
TrMDHc10	:	-----	:
TrMDHc11	:	-----	:
TrMDHc12	:	-----	:
TrMDHc13	:	-----	:
TrMDHc14	:	-----	:
TrMDHc15	:	-----	:
TrMDHc16	:	-----	:
TrMDHc17	:	TTGNCANCGATACACANCCCCC	:

465

Figure 64 Consensus contig nucleotide sequence of TrMDHd

TrMDHd : GGGTAGGCGGAGATTTNAACCCATTTTCCTCTTAAATCTCTCTCAACTTCTCTTTCCATT : 60

TrMDHd : CCCATTACCATTTCATTCCCAGAGGTCGAGATGGCAGCATCAGCAGCAGCTACTTTTACTA : 120

TrMDHd : TTGGAACTGCCCAAACAGGGAGGCCACTTCCTCAATCAAACCCCTTTTGGTTTGAAAGTCA : 180

TrMDHd : ATTCCCAGGTAAATTTTAAGACCTTCTCTGGTCTCAAGGCCATGTCATCTCTAAGATGCG : 240

TrMDHd : AGTCTGAATCATCTTTCTTTGGCAACGAACTAGTGCTGCTCTGCGTGCAACTTTTGCAC : 300

TrMDHd : CCAAAGCTCAAAAGGAAAACCAAAACATCAACCGCAATTGTCATCCTCAGGCATCCTACA : 360

TrMDHd : AAGTGGCGGTTCTTGGTGCTGCAGGAGGAATTGGTCAGCCACTGGCACTTCTCATTAAGA : 420

TrMDHd : TGTGCGCTTTGGTTTCCGACCTGCATCTTTATGATATCGCGAATGTTAAGGGAGTTGCTG : 480

TrMDHd : CTGATATCAGTCATTGCAACACTCCTTCAAAGGTTTGGATTTCACAGGTGCTTCTGAGT : 540

TrMDHd : TGGCAAATTGTTTGAAAGGTGTGGATGTAGTTGTTATACCTGCTGGTGTTCCCAGAAA : 598

Figure 65 Deduced amino acid sequence of TrMDhd

TrMDhd : MAASAAATFTIGTAQTGRPLPQSNPFGLKVNSQVNFKTFSGLKAMSSLRCESESSFFGNE : 60

TrMDhd : TSAALRATFAPKAQKENQNINRNLHPQASYKVAVLGAAGGIGQPLALLIKMSPLVSDLHL : 120

TrMDhd : YDIANVKGVAADISHCNTPSKVLDFTGASELANCLKGVDVVVIPAGVPR : 169

Figure 66 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHd

	* 20 * 40 * 60	
TrMDHd1 :	GNGTAGGCGGAGATTNNAAACCATTTTCCTCTTAAATCTCTCTNAACTTCTCTTTCCATT	: 60
TrMDHd2 :	-GTTTAGGCGGAGATTNNAAACCATTTTCCTCTTAAATCTCTCTC-ACCTTCTCTTTCCATT	: 58
TrMDHd3 :	-----GGGAGATTNNAAACCATTTTCCTCTTAAATCTCTC-CGACTTCTCTGTTCCATT	: 52
	* 80 * 100 * 120	
TrMDHd1 :	CCCATTACCATTCATTCCCAGAGGTCGAGATGGCAGCATCAGCAGCAGCTACTTTTACTA	: 120
TrMDHd2 :	CCCATTACCATTCATTCCCAGAGGTCGAGATGGCAGCATCAGCAGCAGCTACTTTTACTA	: 118
TrMDHd3 :	CCCATTACCATTCATTCCCAGAGGTCGAGATGGCAGCATCAGCAGCAGCTACTTTTACTA	: 112
	* 140 * 160 * 180	
TrMDHd1 :	TTGGAAGTGCACAAACAGGGAGGCCACTTCCTCAATCAAACCCCTTTGGTTTGAAAGTCA	: 180
TrMDHd2 :	TTGGAAGTGCACAAACAGGGAGGCCACTTCCTCAATCAAACCCCTTTGGTTTGAAAGTCA	: 178
TrMDHd3 :	TTGGAAGTGCACAAACAGGGAGGCCACTTCCTCAATCAAACCCCTTTGGTTTGAAAGTCA	: 172
	* 200 * 220 * 240	
TrMDHd1 :	ATTCCCAGGTTAATTTTAAGACCTTCTCTGGTCTCAAGGCCATGTCACTCTAAGATGCG	: 240
TrMDHd2 :	ATTCCCAGGTTAATTTTAAGACCTTCTCTGGTCTCAAGGCCATGTCACTCTAAGATGCG	: 238
TrMDHd3 :	ATTCCCAGGTTAATTTTAAGACCTTCTCTGGTCTCAAGGCCATGTCTCTCTAAGATGCG	: 232
	* 260 * 280 * 300	
TrMDHd1 :	AGTCTGAATCATCTTTCTTTGGCAACGAAACTAGTGCTGCTCTGCGTGCAACTTTTGCAC	: 300
TrMDHd2 :	AGTCTGAATCATCTTTCTTTGGCAACGAAACTAGTGCTGCTCTGCGTGCAACTTTTGCAC	: 298
TrMDHd3 :	AGTCTGAATCATCTTTCTTTGGCAACGAAACTAGTGCTGCTCTGCGTGCAACTTTTGCAC	: 292
	* 320 * 340 * 360	
TrMDHd1 :	CCAAAGCTCAAAAGGAAAACCAAAACATCAACCGCAATTGTCATCCTCAGGCATCCTACA	: 360
TrMDHd2 :	CCAAAGCTCAAAAGGAAAACCAAAACATCAACCGCAATTGTCATCCTCAGGCATCCTACA	: 358
TrMDHd3 :	CCAAAGCTCAAAAGGAAAACCAAAACATCAACCGCAATTGTCATCCTCAGGCATCCTACA	: 352
	* 380 * 400 * 420	
TrMDHd1 :	AAGTGGCGGTTCTTGGTGCTGCAGGAGGAATTGGTCAGCCACTGGCAGTTCTCATTAAAGA	: 420
TrMDHd2 :	AAGTGGCGGTTCTTGGTGCTGCAGGAGGAATTGGTCAGCCACTGGCAGTTCTCATTAAAGA	: 418
TrMDHd3 :	AAGTGGCGGTTCTTGGTGCTGCAGGAGGAATTGGTCAGCCACTGGCAGTTCTCATTAAAGA	: 412
	* 440 * 460 * 480	
TrMDHd1 :	TGTCGCCTTTTGGTTTCCGACCTGCATCTTTATGATATCGCGAATGTTAAGGGAGTTGCTG	: 480
TrMDHd2 :	TGTCGCCTTTTGGTTTCCGACCTGCATCTTTATGATATCGCGAATGTTAAGGGAGTTGCTG	: 478
TrMDHd3 :	TGTCGCCTTTTGGTTTCCGACCTGCATCTTTATGATATCGCGAATGTTAAGGGAGTTGCTG	: 472
	* 500 * 520 * 540	
TrMDHd1 :	CTGATATCAGTCATTGCAACACTCCTTCAAAGGTTTGGATTTACAGGTGCTTCTGAGT	: 540
TrMDHd2 :	CTGATATCAGTCATTGCAACACTCCTTCAAAGGTTTGGATTTACAGGTGCTTCTGAGT	: 538
TrMDHd3 :	CTGATATCAGTCATTGCAACACTCCTTCAAAGGTTTGGATTTACAGGTGCTTCTGAGT	: 532
	* 560 * 580 * 600	
TrMDHd1 :	TGGCAAATTGTTTG-----	: 554
TrMDHd2 :	TGGCAAATTGTTTGAAAGGTGTGGATGTAGTTGTTATACCTGCTGGTGTTCCAG---	: 593
TrMDHd3 :	TAGCAAATTGTTTGAAAGGTGTGGATGTGTTGTTATACCTGCTGGTGTTCCAGAGAAA	: 590

Figure 67 Consensus contig nucleotide sequence of TrMDHe

```

      *           20           *           40           *           60
TrMDHe : TTNTNTTTATTTTATGTTTTTNCCTCCTACATATAACTCTTNACTTNGCATACACTGTG : 60

      *           80           *           100          *           120
TrMDHe : TCTCTCAATTATTATTAGTCCTTAGAAAATGGAAGCACATGCAGCTGGAGCCAATCAGAGG : 120

      *           140          *           160           *           180
TrMDHe : ATTGCAAGAATCTCTGCTCATCTTCAACCTCCAAATTTCCAGGAAGGAGGTGATGTTGCA : 180

      *           200          *           220           *           240
TrMDHe : ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 240

      *           260          *           280           *           300
TrMDHe : GGGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT : 300

      *           320          *           340           *           360
TrMDHe : TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCAGTCTGATGTTAGTCAC : 360

      *           380          *           400           *           420
TrMDHe : ATTGACACCGGTGCTGTGGTTTCGTGGCTTTCTAGGGCAGGCACAACCTTGAGAATGCACCT : 420

      *           440          *           460           *           480
TrMDHe : ACAGGCATGGACTTGGTTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG : 480

      *           500          *           520           *           540
TrMDHe : GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG : 540

      *           560          *           580           *           600
TrMDHe : AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT : 600

      *           620          *           640           *           660
TrMDHe : GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATGATCCAAAGCGACTTTTAGGGGTTACA : 660

      *           680          *           700           *           720
TrMDHe : ACCCTCGATGTTGTGAGGGCAAATACCTTTGTGGCAGAAGTACTTGGTGTGGATCCAAGA : 720

      *           740          *           760           *           780
TrMDHe : GAGGTTGATGTTCCAGTGGTAGGAGGGCACGCAGGAGTCACAATATTACCTCTTTTGTCA : 780

      *           800          *           820           *           840
TrMDHe : CAGGTTAAGCCTCCCAGTAGCTTCACCGCAGAAGAAACCGAATACCTGACAAANCGCATT : 840

      *           860          *           880           *           900
TrMDHe : CAAAANGGCGGAACACAAGTTGTTGAGGCAAAGGCTGGGGCTGGTTTCGGCAACACTANTN : 900

      *           920          *           940           *           960
TrMDHe : ATGGCCTATGCAGCTGCCAAGTTTGCTAACGCATGCCTCCGTGGCTTGAAAGGAGAAGCC : 960

```

* 980 * 1000 * 1020
rMDHe : GGGATAGTGGAGTGTGCTTTTGTGATTCTCAGGTTACGGAACTTCCTTTCTTTGCAGCC : 1020

* 1040 * 1060 * 1080
TrMDHe : AAGGTTTCGTCTTGGTCGCGGTGGAGCAGAAGAGATATCAACTTGGTCCCCTTAATGAG : 1080

* 1100 * 1120 * 1140
TrMDHe : TATGAGAGGATTGGATTAGAAAAAGCGAAGAAAGAGTTAGCAGGAAGCATCCAGAAGGGA : 1140

* 1160 * 1180 * 1200
TrMDHe : GTAGAATTCATCAAAAAAAAAAAGATAAGGAAAAATTAGTTTGTATTGNCTCTTTCT : 1200

* 1220 *
TrMDHe : ATATCTATAAAGAACTTGTGTAATAATTCC : 1230

Figure 68 Deduced amino acid sequence of TrMDHe

TrMDHe : MEAHAAGANQRIARISAHLPNPFQEGGDVAISKANCRAGGAPGFKVAILGAAGGIGQS : 60

TrMDHe : LSLLLKINPLVSVLHLYDVVNTPGVTADVSHIDTGAVVRGFLGQAQLENALTGMDLVVIP : 120

TrMDHe : AGVPRKPGMTRDDLKINAGIVRTLSEGIKSCPNNAIVNLISNPNSTVPPIAAEVFKKAG : 180

TrMDHe : TYDPKRLLGVTTLDVVRANTFVAEVLGVDPREVDVPVVGHHAGVTILPLLSQVKPPSSFT : 240

TrMDHe : AEETEYLTXRIQXGGTQVVEAKAGAGSATLMAYAAAKFANACLRGLKGEAGIVECAFDVS : 300

TrMDHe : QVTELPFFFAAKVRLGRGGAEIYQLGPLNEYERIGLEKAKKELAGSIQKGVEFIKKKXR : 359

Figure 69 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHe.

		*	20	*	40	*	60	
TrMDHe1	:	TTNTNTTTTATTTTATGTTTTTNCCTCCTACATATAACTCTTNACTTNGCATACACTCTG	:	60				
TrMDHe2	:	-----	:	3				
TrMDHe3	:	-----	:	3				
TrMDHe4	:	-----	:	-				
TrMDHe5	:	-----	:	-				
TrMDHe6	:	-----	:	-				
TrMDHe7	:	-----	:	-				
TrMDHe8	:	-----	:	-				
TrMDHe9	:	-----	:	-				
TrMDHe10	:	-----	:	-				
		*	80	*	100	*	120	
TrMDHe1	:	TCTCT-AATTATTATTAGTCCTTGAAATGGAAGCACATGCAGCTGGTACCAATCAGAGG	:	119				
TrMDHe2	:	TCTCTCAATTATTATTAGTCCTTAGAAATGGAAGCACATGCAGCTGGTGCCAATCAGAGG	:	63				
TrMDHe3	:	TCTCTCAATTATTATTAGTCCTTAGAAATGGAAGCACATGCAGCTGGAGCCAATCAGAGG	:	63				
TrMDHe4	:	-----GNAGTCCTTANAAATGGAAGCACATGCAGCTGGAGCC-ATC-GAGG	:	44				
TrMDHe5	:	-----GAGAAATGGAAGCACATGCAGCTGGAGCCAATCAGAGG	:	38				
TrMDHe6	:	-----CCANTGCAGCTGGTGGCCANTNNAGG	:	26				
TrMDHe7	:	-----	:	-				
TrMDHe8	:	-----	:	-				
TrMDHe9	:	-----	:	-				
TrMDHe10	:	-----	:	-				
		*	140	*	160	*	180	
TrMDHe1	:	ATTGCAAGAATCTCTGCTCATCTTCAAGCCTCCAAATTTCCAGGAAGGAGGTGATGTTGCA	:	179				
TrMDHe2	:	ATTGCAAGAATCTCTGCTCATCTTCAACCTCCAAATTTCCAGGAAGGAGGTGATGTTGCA	:	123				
TrMDHe3	:	ATTGCAAGAATCTCTGCTCATCTTCAACCTCCAAATTTCCAGGAAGGAGGTGATGTTGCA	:	123				
TrMDHe4	:	ATTGCAAGAATCTCTGCTCATCTTC-CCTCCAAATTTCCAGGAAGGAAGTGATGTGGCA	:	103				
TrMDHe5	:	ATTGCAAGAATCTCTGCTCATCTTCAACCTCCAAATTTCCAGGAAGGAGGTGATGTTGCA	:	98				
TrMDHe6	:	ATTGC-AGAATCTCTGCTCATCTT-NACCTCC-AATTTCCAGGAAGGAGGTGATGTTGCA	:	83				
TrMDHe7	:	-----	:	-				
TrMDHe8	:	-----	:	-				
TrMDHe9	:	-----	:	-				
TrMDHe10	:	-----	:	-				
		*	200	*	220	*	240	
TrMDHe1	:	ATTAGCAAAGCTAACTGCAGAGCAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG	:	239				
TrMDHe2	:	ATTAGCAAAGCTAACTGCAGAGCAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG	:	183				
TrMDHe3	:	ATTAGCAAAGCTAACTGCAGAGCAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG	:	183				
TrMDHe4	:	ATTAGCAAAGCTAACTGCAGAGCAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG	:	163				
TrMDHe5	:	ATTAGCAAAGCTAACTGCAGAGCAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG	:	158				
TrMDHe6	:	ATTAGCAAAGCTAACTGCAGAGCAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG	:	143				
TrMDHe7	:	-----	:	-				
TrMDHe8	:	-----	:	-				
TrMDHe9	:	-----	:	-				
TrMDHe10	:	-----	:	-				

	*	260	*	280	*	300	
TrMDHe1	:	GGGGCTGCTGGTGGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT				:	299
TrMDHe2	:	GGGGCTGCTGGTGGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT				:	243
TrMDHe3	:	GGGGCTGCTGGTGGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT				:	243
TrMDHe4	:	GGGGCTGCTGGTGGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT				:	223
TrMDHe5	:	GGGGCTGCTGGTGGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT				:	218
TrMDHe6	:	GGGGCTGCTGGTGGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT				:	203
TrMDHe7	:	-----				:	-
TrMDHe8	:	-----				:	-
TrMDHe9	:	-----				:	-
TrMDHe10	:	-----				:	-

	*	320	*	340	*	360	
TrMDHe1	:	TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC				:	359
TrMDHe2	:	TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC				:	303
TrMDHe3	:	TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC				:	303
TrMDHe4	:	TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC				:	283
TrMDHe5	:	TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC				:	278
TrMDHe6	:	TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC				:	263
TrMDHe7	:	-----				:	-
TrMDHe8	:	-----				:	-
TrMDHe9	:	-----				:	-
TrMDHe10	:	-----				:	-

	*	380	*	400	*	420	
TrMDHe1	:	ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACCTTGAGAATGCACTT				:	419
TrMDHe2	:	ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACCTTGAGAATGCACTT				:	363
TrMDHe3	:	ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACCTTGAGAATGCACTT				:	363
TrMDHe4	:	ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACCTTGAGAATGCACTT				:	343
TrMDHe5	:	ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACCTTGAGAATGCACTT				:	338
TrMDHe6	:	ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACCTTGAGAATGCACTT				:	323
TrMDHe7	:	-----				:	-
TrMDHe8	:	-----				:	-
TrMDHe9	:	-----				:	-
TrMDHe10	:	-----				:	-

	*	440	*	460	*	480	
TrMDHe1	:	ACAGGCATGGACTTGGTTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG				:	479
TrMDHe2	:	ACAGGCATGGACTTGGTTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG				:	423
TrMDHe3	:	ACAGGCATGGACTTGGTTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG				:	423
TrMDHe4	:	ACAGGCATGGACTTGGTTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG				:	403
TrMDHe5	:	ACAGGCATGGACTTGGTTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG				:	398
TrMDHe6	:	ACAGGCATGGACTTGGTTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG				:	383
TrMDHe7	:	ACAGGCATGGACTTGGTTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG				:	82
TrMDHe8	:	-----				:	-
TrMDHe9	:	-----				:	-
TrMDHe10	:	-----				:	-

	*	500	*	520	*	540	
TrMDHe1	:	GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG				:	539
TrMDHe2	:	GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG				:	483
TrMDHe3	:	GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG				:	483
TrMDHe4	:	GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG				:	463
TrMDHe5	:	GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG				:	458
TrMDHe6	:	GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG				:	443
TrMDHe7	:	GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG				:	142
TrMDHe8	:	-----				:	-
TrMDHe9	:	-----				:	-
TrMDHe10	:	-----				:	-

	*	560	*	580	*	600	
TrMDHe1	:	AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTC		CACTGTGCCAATT	:	599	
TrMDHe2	:	AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTC		CACTGTGCCAATT	:	543	
TrMDHe3	:	AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTC		CACTGTGCCAATT	:	543	
TrMDHe4	:	AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTC		CACTGTGCCAATT	:	523	
TrMDHe5	:	AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTC		CACTGTGCCAATT	:	518	
TrMDHe6	:	AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTC		CACTGTGCCAATT	:	503	
TrMDHe7	:	AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTC		CACTGTGCCAATT	:	202	
TrMDHe8	:	-----		-----	:	-	
TrMDHe9	:	-----		-----	:	-	
TrMDHe10	:	-----		-----	:	-	

	*	620	*	640	*	660	
TrMDHe1	:	GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATGATCCAAAGCGACTTTTAN		GGGTACA	:	659	
TrMDHe2	:	GCTGCTGAGGTTTTCAAGAAAGCCGGTACAT		-----	:	574	
TrMDHe3	:	GCTGCTGAGGTTTTCAAGAAAGCCGGTACATAT		-----	:	576	
TrMDHe4	:	GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATGATCCAAAGCGACTTTT		AGGAGTTACA	:	583	
TrMDHe5	:	GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATGATCCAAAGCGACTTTT		AGGAGTTACA	:	578	
TrMDHe6	:	GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATGATCCAAAGCGACTTTT		AGGAGTTACA	:	555	
TrMDHe7	:	GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATGATCCAAAGCGACTTTT		AGGAGTTACA	:	262	
TrMDHe8	:	-----		TATGATCC-AGCGCGACTTTTAGG-GGTACA	:	28	
TrMDHe9	:	-----		-----	:	-	
TrMDHe10	:	-----		-----	:	-	

	*	680	*	700	*	720	
TrMDHe1	:	ACCCTCGATGNTGT		-----		-----	: 673
TrMDHe2	:	-----		-----		-----	: -
TrMDHe3	:	-----		-----		-----	: -
TrMDHe4	:	ACCCTCGATG		-----		-----	: -
TrMDHe5	:	ACCCTNGATGTTGNGAGGGCAAATACCTTTGTGGCANAAG-NCTTGNGTTGANCCGANA		-----		-----	: 593
TrMDHe6	:	-----		-----		-----	: 637
TrMDHe7	:	ACCCTCGATGTTGTGAGGGCAAATACCTTTGTGGCAGAAGTACTTGGTGTGATCCAAGA		-----		-----	: -
TrMDHe8	:	ACCCTCGATGTTGTGAGGGCAAATACCTTTGTGGCAGAAGTACTTGGTGTGATCCAAGA		-----		-----	: 322
TrMDHe9	:	-----		-----		-----	: 88
TrMDHe10	:	-----		-----		-----	: -

	*	740	*	760	*	780	
TrMDHe1	:	-----		-----		-----	: -
TrMDHe2	:	-----		-----		-----	: -
TrMDHe3	:	-----		-----		-----	: -
TrMDHe4	:	-----		-----		-----	: -
TrMDHe5	:	NAGGCTNATNTTCCANTGGTAGGAGGGGCCCCNCGANT-ACAAATATACC-CITTTTIT		-----		-----	: 693
TrMDHe6	:	-----		-----		-----	: -
TrMDHe7	:	GAGGTTGATGTTCCAGNNGGTAGGAGGGCACGCANAGACT-ACAATATTACCTCTTTTGTCA		-----		-----	: 381
TrMDHe8	:	GAGGTTGATGTTCCAGTGGTAGGAGGGCACGCAGGAGTCACAATATTACCTCTTTTGTCA		-----		-----	: 148
TrMDHe9	:	-----		-----		-----	: -
TrMDHe10	:	-----		-----		-----	: -

	*	800	*	820	*	840	
TrMDHe1	:	-----		-----		-----	: -
TrMDHe2	:	-----		-----		-----	: -
TrMDHe3	:	-----		-----		-----	: -
TrMDHe4	:	-----		-----		-----	: -
TrMDHe5	:	-----		-----		-----	: -
TrMDHe6	:	-----		-----		-----	: -
TrMDHe7	:	CAGGTTAAGCCTNCCAGTANCTT-ACCGNAGAAANAAACCGAATACCTGACANANCGNATT		-----		-----	: 440
TrMDHe8	:	CAGGTTAAGCCTCCCAGTAGCTTCACITGCAGAAGAAACCGAATACCTGACAAATCGCATT		-----		-----	: 208
TrMDHe9	:	-----		-----		-----	: -
TrMDHe10	:	-----		-----		-----	: -

	*	860	*	880	*	900	
TrMDHe1	:	-----		-----		-----	-
TrMDHe2	:	-----		-----		-----	-
TrMDHe3	:	-----		-----		-----	-
TrMDHe4	:	-----		-----		-----	-
TrMDHe5	:	-----		-----		-----	-
TrMDHe6	:	-----		-----		-----	-
TrMDHe7	:	CAAAANGGCGGAACACAAGT		GTTGAGGCAAAG		-----	473
TrMDHe8	:	CAAAATGGTGGGAACA		GAAGTTGTTGAGGCAAAGGCTGGGGCTGGTTGGGCAACACTANT		-----	268
TrMDHe9	:	-----		GTTGTTGAGGCAAAGGCTGGGGCTGGTTGGGCAACACTANTN		-----	42
TrMDHe10	:	-----		TTGTTGAGGNAAGGCTGGGGCTGGTTGGG		NAC-CT-NTN	38

	*	920	*	940	*	960	
TrMDHe1	:	-----		-----		-----	-
TrMDHe2	:	-----		-----		-----	-
TrMDHe3	:	-----		-----		-----	-
TrMDHe4	:	-----		-----		-----	-
TrMDHe5	:	-----		-----		-----	-
TrMDHe6	:	-----		-----		-----	-
TrMDHe7	:	-----		-----		-----	-
TrMDHe8	:	ATGGC		TATGCAGCTGCCAAGTTTGCTAACGCATGCCTCCGTGGCTTGAAAGGAGAAGCC		-----	328
TrMDHe9	:	ATGGCCTATGCAGCTGCCAAGTTTGCTAACGCATGCCTCCGTGGCTTGAAAGGAGAAGCC		-----		-----	102
TrMDHe10	:	ATGGCCTATGCAGCTGCC		AGTTTGCTAACGCATGCCTCCGTGGCTTGAAAGGAGAAGCC		-----	97

	*	980	*	1000	*	1020	
TrMDHe1	:	-----		-----		-----	-
TrMDHe2	:	-----		-----		-----	-
TrMDHe3	:	-----		-----		-----	-
TrMDHe4	:	-----		-----		-----	-
TrMDHe5	:	-----		-----		-----	-
TrMDHe6	:	-----		-----		-----	-
TrMDHe7	:	-----		-----		-----	-
TrMDHe8	:	GGGATAGTGGAGTGTGCTTTTGTGATTCTCAGGTTACGGAAC		TTCCGTTTCTTTGCAGCC		-----	388
TrMDHe9	:	GGGATAGTGGAGTGTGCTTTTGTGATTCTCAGGTTACGGAAC		TTCCGTTTCTTTGCAGCC		-----	162
TrMDHe10	:	GGGATAGTGGAGTGTGCTTTTGTGATTCTCAGGTTACGGAAC		TTCCGTTTCTTTGCAGCC		-----	157

	*	1040	*	1060	*	1080	
TrMDHe1	:	-----		-----		-----	-
TrMDHe2	:	-----		-----		-----	-
TrMDHe3	:	-----		-----		-----	-
TrMDHe4	:	-----		-----		-----	-
TrMDHe5	:	-----		-----		-----	-
TrMDHe6	:	-----		-----		-----	-
TrMDHe7	:	-----		-----		-----	-
TrMDHe8	:	AAGGTTTCGTCTTGGTCGCGGTGGAGCAGAAGAGATATAC		CAACTTGGTCCCCTTAATGAG		-----	448
TrMDHe9	:	AAGGTTTCGTCTTGGTCGCGGTGGAGCAGAAGAGATATATCAACTTGGTCCCCTTAATGAG		-----		-----	222
TrMDHe10	:	AAGGTTTCGTCTTGGTCGCGGTGGAGCAGAAGAGATATATCAACTTGGTCCCCTTAATGAG		-----		-----	217

	*	1100	*	1120	*	1140	
TrMDHe1	:	-----		-----		-----	-
TrMDHe2	:	-----		-----		-----	-
TrMDHe3	:	-----		-----		-----	-
TrMDHe4	:	-----		-----		-----	-
TrMDHe5	:	-----		-----		-----	-
TrMDHe6	:	-----		-----		-----	-
TrMDHe7	:	-----		-----		-----	-
TrMDHe8	:	TATGAGAGGATTGGG		TTTGAAAAAGCGAAGAA		TGAGTTAGCGGGAAGCATCCAGAAGGGA	508
TrMDHe9	:	TATGAGAGGATTGGATTAGAAAAAGCGAAGAAAGAGTTAGCAGGAAGCATCCAGAAGGGA		-----		-----	282
TrMDHe10	:	TATGAGAGGATTGGATTAGAAAAAGCGAAGAAAGAGTTAGCAGGAAGCATCCAGAAGGGA		-----		-----	277

	*	1160	*	1180	*-	1200	
TrMDHe1	:	-----	:	-----	:	-----	-
TrMDHe2	:	-----	:	-----	:	-----	-
TrMDHe3	:	-----	:	-----	:	-----	-
TrMDHe4	:	-----	:	-----	:	-----	-
TrMDHe5	:	-----	:	-----	:	-----	-
TrMDHe6	:	-----	:	-----	:	-----	-
TrMDHe7	:	-----	:	-----	:	-----	-
TrMDHe8	:	GTAGAATTCATCAGAAAAAAGTCAGATAAGGAAAAATTAGTTTTGTATTGNCTCTTTCT					: 568
TrMDHe9	:	GTAGAATTCATCAGAAAAAANAA					: 306
TrMDHe10	:	GTAGAATTCATCAAAAAAAAAAN					: 299

	*	1220	*	
TrMDHe1	:	-----	:	-
TrMDHe2	:	-----	:	-
TrMDHe3	:	-----	:	-
TrMDHe4	:	-----	:	-
TrMDHe5	:	-----	:	-
TrMDHe6	:	-----	:	-
TrMDHe7	:	-----	:	-
TrMDHe8	:	ATATCTATAAAGAACTTGTGTAATAATTCC		: 598
TrMDHe9	:	-----	:	-
TrMDHe10	:	-----	:	-

Figure 70 Consensus contig nucleotide sequence of TrMDHf

```

      *           20           *           40           *           60
TrMDHf : GNN TACNGCTATC NACCTTCTTTCTTATACAATAATNATAGATAAATTCATCTGCTAAA : 60

      *           80           *           100          *           120
TrMDHf : TTATGGAGCCAAATTCAGATGCAAATCAACGAATCGCAAGAATCTCCGGCCACCTAAATC : 120

      *           140          *           160           *           180
TrMDHf : CTCCCAATTTCAAGATGAATGAACATGGTGATTCTTCTTTGACAAGTTTCCATTGCCGTG : 180

      *           200          *           220           *           240
TrMDHf : CAAAAGGTGGAGCACCTGGATTCAAAGTTGCAATTTTAGGTGCTGCTGGTGGCATAGGTC : 240

      *           260          *           280           *           300
TrMDHf : AACCTCTTTCAATGTTGATGAAGATGAATCCTTTGGTTT NAGTTCTTCATCTTTATGATG : 300

      *           320          *           340           *           360
TrMDHf : TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCATATGGATACTGCTGCTGTTGTTTC : 360

      *           380          *           400           *           420
TrMDHf : GAGGGTTTTTTGGGGCAAATCAGCTTGAGGATGCACCTTACAGGTATGGATTGGTAATCA : 420

      *           440          *           460           *           480
TrMDHf : TTCCTGCCGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG : 480

      *           500          *           520           *           540
TrMDHf : CCGGGATCGTTAAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAAGGCGATTGTCA : 540

      *           560          *           580           *           600
TrMDHf : ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTTCAAAGAG : 600

      *           620          *           640           *           660
TrMDHf : CCGGTACTTATGATCCCAAGAGACTTTTGGGAGTGACAATGCTTGATGTGGTTCGGGCCA : 660

      *           680          *           700           *           720
TrMDHf : ATACGTTTGTGGCTGAAGTTCTTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCTG : 720

      *           740          *           760           *           780
TrMDHf : GAGGACATGCCGGAATCACCATTTTACCTCTGCTTTCTCAGGTAAACCACATTCCTCTT : 780

      *           800          *           820           *           840
TrMDHf : TCACGACAAAGGAAATTGAGTACTTGACAGATCGCATAAAAACGGTGGAAGTTG : 840

      *           860
TrMDHf : TTGAGGCCAAAGCTGGAGCTGGCTCT : 866

```

Figure 71 Deduced amino acid sequence of TrMDHf

TrMDHf : MEPNSDANQRIARISGHLNPPNFKMNEHGDSSLTSFHCRAKGGAPGFKVAILGAAGGIGQ : 60

TrMDHf : PLSMLMKMNPLVXVLHLYDVVNTPGVTSDISHMDTAAVVRGFLGQNQLEDALTGMDLVII : 120

TrMDHf : PAGVPRKPGMTRDDLFNINAGIVKTLCEALAKRCPKAIVNVISNPVNSTVPIAAEVFKRA : 180

TrMDHf : GTYDPKRLLGVTMLDVVRANTFVAEVLGLDPRDVPVVGGHAGITILPLLSQVKPHSSF : 240

TrMDHf : TTKEIEYLTDRIQNGGTEVVEAKAGAGS : 268

Figure 72 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHf

	* 20 * 40 * 60	
TrMDHf1 :	GNNTACNGCTATCNACCCTTCTTTCTTATACAATAATNATAGATAAAATTCATCTGCTAAA	: 60
TrMDHf2 :	-----	: -
TrMDHf3 :	-----	: -
	* 80 * 100 * 120	
TrMDHf1 :	TTATGGAGCCAAATTCAGATGCAAATCAACGAATCGCAAGAATCTCCGCGCCACCTAAATC	: 120
TrMDHf2 :	-----	: -
TrMDHf3 :	-----	: -
	* 140 * 160 * 180	
TrMDHf1 :	CTCCCAATTTCAAGATGAATGAACATGGTGATTCTTCTTTGACAAGTTTCCATTGCCGTG	: 180
TrMDHf2 :	-----	: -
TrMDHf3 :	-----	: -
	* 200 * 220 * 240	
TrMDHf1 :	CAAAAGGTGGAGCACCTGGATTCAAAGTTGCAATTTTAGGTGCTGCTGGTGGCATAGGTC	: 240
TrMDHf2 :	-----GTGNCATAGGTN	: 12
TrMDHf3 :	-----	: -
	* 260 * 280 * 300	
TrMDHf1 :	AACCTCTTTCAATGTTGATGAAGATGAATCCCTTGGTTT-AGTTCCTGATCTTTATGATG	: 299
TrMDHf2 :	ACCCTCTTT-NATGTTGATGAAGATGAATCCTATGGTTT-AGTTCCTGATCTTTATGATG	: 70
TrMDHf3 :	-----TTTGGTTTNGTTCTTATNCTTTATGATG	: 29
	* 320 * 340 * 360	
TrMDHf1 :	TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCAATGGATACTGCTGCTGTTGTTTC	: 359
TrMDHf2 :	TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCATATGGATACTGCTGCTGTTGTTTC	: 130
TrMDHf3 :	TTG-TAATACTCCTGGTG-TACTTCTGATATTAGT-ATATGGATACTGCTGCTGTTGTTTC	: 86
	* 380 * 400 * 420	
TrMDHf1 :	GAGGATTTTTTGGGGCAAAATCAGCTTGAGGATGCACCTACAGGTATGGATTGGTAATCA	: 419
TrMDHf2 :	GAGGGTTTTTGGGGCAAAATCAGCTTGAGGATGCACCTACAGGTATGGATTGGTAATCA	: 190
TrMDHf3 :	GAGGGTTTTTGGGGCAAAATCAGCTTGAGGATGCACCTACAGGTATGGATTGGTAATCA	: 146
	* 440 * 460 * 480	
TrMDHf1 :	TTCTTGCGGGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG	: 479
TrMDHf2 :	TTCTTGCGGGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG	: 250
TrMDHf3 :	TTCTTGCGGGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG	: 206
	* 500 * 520 * 540	
TrMDHf1 :	CCGGGATCGTTAAACACTCTGTGAAGCAATTGCAGCGATGTCCTAAGGCGATTGTCA	: 539
TrMDHf2 :	CCGGGATCGTTAAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAAGGCGATTGTCA	: 310
TrMDHf3 :	CCGGGATCGTTAAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAAGGCGATTGTCA	: 266
	* 560 * 580 * 600	
TrMDHf1 :	ACGTGATTAGTAATCCGGTTAACTCCACTGTCC-----	: 572
TrMDHf2 :	ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTCAAAGAG	: 370
TrMDHf3 :	ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTCAAAGAG	: 326

	*	620	*	640	*	660	
TrMDHf1 :	-----						-
TrMDHf2 :	CCGGTACTTATGATCCCAAGAGACTTTTGGGAGTGACAATGCTTGATGTGGTTCGGGGCCA						: 430
TrMDHf3 :	CCGGTACTTATGATCCCAAGAGACTTTTGGGAGTGACAATGCTTGATGTGGTTCGGGGCCA						: 386

	*	680	*	700	*	720	
TrMDHf1 :	-----						-
TrMDHf2 :	ATACGTTTGTGGCTGAAGTTCTTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCTG						: 490
TrMDHf3 :	ATACGTTTGTGGCTGAAGTTCTTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCTG						: 446

	*	740	*	760	*	780	
TrMDHf1 :	-----						-
TrMDHf2 :	GAGGACATGCCGGAATCACCATTTTACCTCTGCTTTCTCAGGTTAAACACATTCCTCTT						: 550
TrMDHf3 :	GAGGACATGCCGGAATCACCATTTTACCTCTGCTTTCTCAGGTTAAACACATTCCTCTT						: 506

	*	800	*	820	*	840	
TrMDHf1 :	-----						-
TrMDHf2 :	TCACGACAAAGGAAATTGAGTACTTG-----						: 576
TrMDHf3 :	TCACGACAAAGGAAATTGAGTACTTGACAGATCGCATACAAACGGTGGAACTGAAGTTG						: 566

	*	860	
TrMDHf1 :	-----		-
TrMDHf2 :	-----		-
TrMDHf3 :	TTGAGGCCAAAGCTGGAGCTGGCTCT		: 592

Figure 73 Consensus contig nucleotide sequence of TrMDHg

TrMDHg : GTAGGCAGCATCTAACAGCACAAATGAACATGGAAATGTTTGCTTTGGAAATTATGGACAA : 60

TrMDHg : TACGGTCCTTAAAAAATCTGTTCTTGTTTTATTTTGTACTTTTGTGTTTGGGAAGATCGT : 120

TrMDHg : TAGATACATGTGTGGTCTTCTCAAAGTTGATAAGGAACCAGTCACTGTATTGGTCACTGG : 180

TrMDHg : TGCTGCAGGACAAATTGGNTATGCTCTTGNTCCAATGATTGCAAGAGGGATGATGCTAGG : 240

TrMDHg : CCCAAATCAACCTGGAATTCTTCATATGCTNGATATTGAACCAGGATTAGAGGCCCTTAA : 300

TrMDHg : AGGGGTGAAGATGGAAGTGAATGATGGTGCCTTCCCACTTCTTAGAGGTGTTGTTGCTAC : 360

TrMDHg : TACGGATGTTGTTGAAGCATGCAAGGATGTTAACATTGCTGTTATGCTTGGTGGATCCCC : 420

TrMDHg : AAGGAAGGAAGGAATGGAAAGAAAAGATGTAATGTCTAAGAATGTTTCAATTTACAAGGC : 480

TrMDHg : TCAAGCTTCAGCTTTGGAGGAGCATGCTGCTGCAGATTGTAAAGTGCTAGTGGTAGCCAA : 540

TrMDHg : TCCAGCAAACACAAATGCTCTAATATTGAAAGAATTTGCTCCATCAATCCCTGAGAAAA : 599

Figure 74 Deduced amino acid sequence of TrMDHg

TrMDhg : MCGLLKVDKEPVTVLVTGAAGQIXYALXPMIARGMMLGPNQPGILHMXDIEPGLEALKGV : 60

TrMDhg : KMELIDGAFPLLRLRGVVATTDVVEACKDVNIAVMLGGSPRKEGMRKDVMSKNVSIYKAQA : 120

TrMDhg : SALEEHAAADCKVLVVANPANTNALILKEFAPSIPEK : 157

Figure 75 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHg

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      *           ~20           *           40           *           60
TrMDHg1 : GTAGGCA[CA]--TAACAGCACAATGAACATGGAAATGTTTGCTTTGGAAATTATGGACAATA : 60
TrMDHg2 : ---GNNGGATCTAACAG-ACAATGAACATGGAAATGTTTGCTTTGGAAATTATGGACAATA : 57

      *           80           *           100           *           120
TrMDHg1 : CGGTCCTTAAAAAATCTGTTCTTGTTTTATTTTGTACTTTTTTGTGTTTGGGAAGATCGTTAGA : 122
TrMDHg2 : CGGTCCTTAAAAAATCTGTTCTTGTTTTATTTTGTACTTTTTTGTGTTTGGGAAGATCGTTAGA : 119

      *           140           *           160           *           180
TrMDHg1 : TACATGTGTGGTCTTCTCAAAGTTGATAAGGAACCAGTCACTGTATTGGTCACTGGTGCTGC : 184
TrMDHg2 : TACATGTGTGGTCTTCTCAAAGTTGATAAGGAACCAGTCACTGTATTGGTCACTGGTGCTGC : 181

      *           200           *           220           *           240
TrMDHg1 : AGGACAAATTGGNTATGCTCTTGNTNCAATGATTGCNANAGGGATGATGCTANGNCCAAATC : 246
TrMDHg2 : AGGACAAATTGGNTATGCTCTTGTTCCAATGATTGCAAGAGGGATGATGCTAGGCCCAAATC : 243

      *           260           *           280           *           300           *
TrMDHg1 : NACCTGGNATTGTTGATATGCTNGNTTTG----- : 276
TrMDHg2 : AACCTGTAATTCTTCATATGCTTGATATTGAACCAGGATTAGAGGCCCTTAAAGGGGTGAAG : 305

      320           *           340           *           360           *
TrMDHg1 : ----- : -
TrMDHg2 : ATGGAAGTGAATGATGGTGCTTTCCCACTTCTTAGAGGTGTTGTTGCTACTACGGATGTTGT : 367

      380           *           400           *           420           *
TrMDHg1 : ----- : -
TrMDHg2 : TGAAGCATGCAAGGATGTTAACATTGCTGTTATGCTTGGTGGATCCCCAAGGAAGGAAGGAA : 429

      440           *           460           *           480           *
TrMDHg1 : ----- : -
TrMDHg2 : TGGAAAGAAAAGATGTAATGTCTAAGAATGTTTCAATTTACAAGGCTCAAGCTTCAGCTTTG : 491

      500           *           520           *           540           *           5
TrMDHg1 : ----- : -
TrMDHg2 : GAGGAGCATGCTGCTGCAGATTGTAAAGTGCTAGTGGTAGCCAATCCAGCAAACACAAATGC : 553

      60           *           580           *
TrMDHg1 : ----- : -
TrMDHg2 : TCTAATATTGAAAGAATTGCTCCATCAATCCCTGAGAAAA : 594

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Figure 76 Consensus contig nucleotide sequence of TrMDHh

```

      *           20           *           40           *           60
TrMDHh : GNNTACNGCTATCNACCCTTCTTTCTTATACAATAATNATAGATAAAATTCATCTGCTAAA : 60

      *           80           *           100          *           120
TrMDHh : TTATGGAGCCAAATTCAGATGCAAATCAACGAATCGCAAGAATCTCCGGCCACCTAAATC : 120

      *           140          *           160          *           180
TrMDHh : CTCCCAATTTCAAGATGAATGAACATGGTGATTCTTCTTTGACAAGTTTCCATTGCCGTG : 180

      *           200          *           220          *           240
TrMDHh : CAAAAGGTGGAGCACCTGGATTCAAAGTTGCAATTTTAGGTGCTGCTGGTGGCATAGGTC : 240

      *           260          *           280          *           300
TrMDHh : AACCTCTTTCAATGTTGATGAAGATGAATCCTTTGGTTNAGTTCTTCATCTTTATGATG : 300

      *           320          *           340          *           360
TrMDHh : TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCATATGGATACTGCTGCTGTTGTTTC : 360

      *           380          *           400          *           420
TrMDHh : GAGGGTTTTTGGGGCAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA : 420

      *           440          *           460          *           480
TrMDHh : TTCCTGCCGGTGTTCCCGGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG : 480

      *           500          *           520          *           540
TrMDHh : CCGGGATCGTTAAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAAGGCGATTGTCA : 540

      *           560          *           580          *           600
TrMDHh : ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTTCAAAGAG : 600

      *           620          *           640          *           660
TrMDHh : CCGGTACTTATGATCCCAAGAGACTTTTGGGAGTGACAATGCTTGATGTGGTTCGGGCCA : 660

      *           680          *           700          *           720
TrMDHh : ATACGTTTGTGGCTGAAGTTCTTGGTCTTGATCCAAGGGATGTGGATGTCCAGTTGTCTG : 720

      *           740          *           760          *           780
TrMDHh : GAGGACATGCCGGAATCACCATTTTACCTCTGCTTTCTCAGGTTAAACCACATTCTCTT : 780

      *           800          *           820          *           840
TrMDHh : TCACGACAAAGGAAATTGAGTACTTGACAGATCGCATACAAAACGGTGGAAGTGAAGTTG : 840

      *           860
TrMDHh : TTGAGGCCAAAGCTGGAGCTGGCTCT : 866

```

Figure 77 Deduced amino acid sequence of TrMDHh

```

      *           20           *           40           *           60
TrMDHh : MEPNSDANQRIARISGHLNPPNFKMNEHGDSSLTSHFCRAKGGAPGFKVAILGAAGGIGQ : 60

      *           80           *           100          *           120
TrMDHh : PLSMLMKMNPLVXVLHLYDVVNTPGVTSDISHMDTAAVVRGFLGQNQLEDALTGMDLVII : 120

      *           140          *           160          *           180
TrMDHh : PAGVPRKPGMTRDDLFNINAGIVKTLCEAIAKRCPKAIVNVISNPVNSTVPIAAEVFKRA : 180

      *           200          *           220          *           240
TrMDHh : GTYDPKRLLGVTMLDVVRANTFVAEVLGLDPRDVPVVGGHAGITILPLLSQVKPHSSF : 240

      *           260
TrMDHh : TTKEIEYLTDRIQNGGTEVVEAKAGAGS : 268
```

Figure 78 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHh

	* 20 * 40 * 60	
TrMDHh1 :	GNNATACNGCTATCNACCCTTCTTTCTTATACAATAATNATAGATAAAATTCATCTGCTAAA	: 60
TrMDHh2 :	-----	: -
TrMDHh3 :	-----	: -
	* 80 * 100 * 120	
TrMDHh1 :	TTATGGAGCCAAATTCAGATGCAAATCAACGAATCGCAAGAATCTCCGGCCACCTAAATC	: 120
TrMDHh2 :	-----	: -
TrMDHh3 :	-----	: -
	* 140 * 160 * 180	
TrMDHh1 :	CTCCCAATTTCAAGATGAATGAACATGGTGATTCTTCTTTGACAAGTTTCCATTGCCCGTG	: 180
TrMDHh2 :	-----	: -
TrMDHh3 :	-----	: -
	* 200 * 220 * 240	
TrMDHh1 :	CAAAAGGTGGAGCACCTGGATTCAAAGTTGCAATTTTAGGGTGCTGCTGGTGGCATAGGTC	: 240
TrMDHh2 :	-----GTGNCATAGGTT	: 12
TrMDHh3 :	-----	: -
	* 260 * 280 * 300	
TrMDHh1 :	AACCTCTTTCAATGTTGATGAAGATGAATCCCTTGTTTT-AGTTCTTCATCTTTATGATG	: 299
TrMDHh2 :	AACCTCTTT-NATGTTGATGAAGATGAATCCCTTGTTTT-AGTTCTTCATCTTTATGATG	: 70
TrMDHh3 :	-----TTTGGTTTNGTTCTTATNCTTTATGATG	: 29
	* 320 * 340 * 360	
TrMDHh1 :	TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCACATGGATACTGCTGCTGTTGTTTC	: 359
TrMDHh2 :	TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCATATGGATACTGCTGCTGTTGTTTC	: 130
TrMDHh3 :	TTG-TAATACTCCTGGTG-TACTTCTGATATTAGT-ATATGGATACTGCTGCTGTTGTTTC	: 86
	* 380 * 400 * 420	
TrMDHh1 :	GAGGTTTTTTGGGGCAAATCAGCTTGAGGATGCACCTTACAGGTATGGATTGCGTAATCA	: 419
TrMDHh2 :	GAGGTTTTTTGGGGCAAATCAGCTTGAGGATGCACCTTACAGGTATGGATTGCGTAATCA	: 190
TrMDHh3 :	GAGGTTTTTTGGGGCAAATCAGCTTGAGGATGCACCTTACAGGTATGGATTGCGTAATCA	: 146
	* 440 * 460 * 480	
TrMDHh1 :	TTCTGCTGGTGTTCCCGGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG	: 479
TrMDHh2 :	TTCTGCCGGTGTTCCCGGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG	: 250
TrMDHh3 :	TTCTGCCGGTGTTCCCGGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG	: 206
	* 500 * 520 * 540	
TrMDHh1 :	CCGGGATCGTTAAACACTCTGTGAAGCAATTGCAAGCGATGTCCTAAGGCGATTGTCA	: 539
TrMDHh2 :	CCGGGATCGTTAAACACTCTGTGAAGCAATTGCAAGCGATGTCCTAAGGCGATTGTCA	: 310
TrMDHh3 :	CCGGGATCGTTAAACACTCTGTGAAGCAATTGCAAGCGATGTCCTAAGGCGATTGTCA	: 266
	* 560 * 580 * 600	
TrMDHh1 :	ACGTGATTAGTAATCCGGTTAACTCCACTGTGCC-----	: 572
TrMDHh2 :	ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTTCAAAGAG	: 370
TrMDHh3 :	ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTTCAAAGAG	: 326

	*	620	*	640	*	660	
TrMDHh1 :	-----						:
TrMDHh2 :	CCGGTACTTATGATCCCAAGAGACTTTGGGAGTGACAATGCTTGATGTGGTTTCGGGCCA						: 430
TrMDHh3 :	CCGGTACTTATGATCCCAAGAGACTTTGGGAGTGACAATGCTTGATGTGGTTTCGGGCCA						: 386

	*	680	*	700	*	720	
TrMDHh1 :	-----						:
TrMDHh2 :	ATACGTTTGTGGCTGAAGTTCTTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCTG						: 490
TrMDHh3 :	ATACGTTTGTGGCTGAAGTTCTTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCTG						: 446

	*	740	*	760	*	780	
TrMDHh1 :	-----						:
TrMDHh2 :	GAGGACATGCCGGAATCACCATTTTACCTCTGCTTTCTCAGGTTAAAGCACATTCCTCTT						: 550
TrMDHh3 :	GAGGACATGCCGGAATCACCATTTTACCTCTGCTTTCTCAGGTTAAAGCACATTCCTCTT						: 506

	*	800	*	820	*	840	
TrMDHh1 :	-----						:
TrMDHh2 :	TCACGACAAAGGAAATTGAGTACTTG-----						: 576
TrMDHh3 :	TCACGACAAAGGAAATTGAGTACTTGACAGATCGCATACAAAACGGTGGAAGTGAAGTTG						: 566

	*	860	
TrMDHh1 :	-----		:
TrMDHh2 :	-----		:
TrMDHh3 :	TTGAGGCCAAAGCTGGAGCTGGCTCT		: 592

Figure 79 Consensus contig nucleotide sequence of TrMDHi

TrMDHi : GNAATCCTCTTTGNCTCCCCTACCCTCCTTTTTTTTCTTCCTTCTTACACCTTCTCTTA : 60

TrMDHi : TCAACTTTCCACCTCTGAACAAACTTCAATCTTTTCTCATTTTCTTATACCCTTTTACA : 120

TrMDHi : AACTTCTTCATAAAGTGTTAGGTTTTTTTTTATTACTCTTTTCAAGAACCACAAAAACAG : 180

TrMDHi : TGTTTCTTGAATTCTTTGGAATTTTTTTTTTCTGCAACCATGGCCTTGGCACACTTAAA : 240

TrMDHi : CAACCCCACTTGCTCAAAAACCTCAACTTCACTCATCACAACCTCTCATTTCTCTCTAGGAC : 300

TrMDHi : TCTCCCTAGGCAATATCACTGTACTTTTGCACCACTTCACAGAACTCAACATGGCAGAAT : 360

TrMDHi : TACTTGTTCTGTTGCACCAAATCAAGTGCAGGCTCCAGCTGTACAATCACAGGATCCCAA : 420

TrMDHi : GAATAAGCCTGATTGCTATGGTGTCTTCTGCCTTACCTATGATTGGAAGGCTGAAGAGGA : 480

TrMDHi : GACAAAATCCTGGAAGAAATTAATCAACATTGCAGTCTCAGGTGCTGCTGGAATGATTTC : 540

TrMDHi : CAATCATCTACTTTTCAAGCTTGCATCTGGTGAAGTTTTTGGCCCAAATCAACCTATTGC : 600

TrMDHi : GCTGAAATTATTAGGATCAGAAAGGTCCTTCCAAGCTCTTGAAGGTG : 647

Figure 80 Deduced amino acid sequence of TrMDHi

TrMDHi : * 20 * 40 * 60
MALAHLNNPTCSKTQLHSSQLSFLSRTLPRQYHCTFAPLHRTQHGRITCSVAPNQVQAPA : 60

TrMDHi : * 80 * 100 * 120
VQSQDPKNKPCYGVFCLTYDLKAEETKSWKKLINIAVSGAAGMISNHLLFKLASGEVF : 120

TrMDHi : * 140
GPNQPIALKLLGSERSFQALEG : 142

Figure 81 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHi

```

      *           20           *           40           *           60
TrMDHi1 : GNAATCCTCTTTGNCTCCCTACCTCCTTTTTTTTCTTCCTTCTTACA-CTTCTCTTCT : 60
TrMDHi2 : -----TTCTTAGACCTTCTCTTAT : 19

      *           80           *           100          *           120
TrMDHi1 : CAACTTTCCACCTCTGAACAAACTTCATCTTTTCTCATTCTTATACCCTTTTAGAAA : 121
TrMDHi2 : -AACTTTTCACCTCTGAACAAA-TT-AACTCTTTCT-ATTTTCTTATACCCTTTTACAAA : 76

      *           140          *           160          *           180
TrMDHi1 : CTTCTTCATAAAGTGTTATTTT-TTTTTTATTACTCTTTTCAAGAAAGACAAAAACAGTGT : 180
TrMDHi2 : CTTCTTCATAAAGTGTTGGTTTTTTTTTTATTACTCTTTTCAAGAACCACAAAAACAGTGT : 137

      *           200          *           220          *           240
TrMDHi1 : TTCTTGAATTCTTTTGAATTTTTTTTTTCTGCAACCATGGCCTTGGGACAGTTAAACAAAT : 241
TrMDHi2 : TTCTTGAATTC-TTGGAA-TTTTTTTTTTCTGCAACCATGGC-TTGGGACACTTAAACAAC : 196

      *           260          *           280          *           300
TrMDHi1 : CCCACTTGCTCAAAAACCTCAACTTCACTCATCACAACCTCTCATTCTTCTCTAGGACTCTCC : 302
TrMDHi2 : CCCACTTGCTCAAAAACCTCAACTTCACTCATCACAACCTCTCATTCTCTCTAGGACTCTCC : 257

      *           320          *           340          *           360
TrMDHi1 : CTAGGCAATATCACTGTACTTTTGCACCACTTCACAGAACTCAACATGGCAGAATTACTTG : 363
TrMDHi2 : CTAGGCAATATCACTGTACTTTTGCACCACTTCACAGAACTCAACATGGCAGAATTACTTG : 318

      *           380          *           400          *           420
TrMDHi1 : TTCTGTTGCACCAAATCAAGTGCAGGCTCCAGCTGTACAATCACAGGATCCCAAGAATAAG : 424
TrMDHi2 : TTCTGTTGCACCAAATCAAGTGCAGGCTCCAGCTGTACAATCACAGGATCCCAAGAATAAG : 379

      *           440          *           460          *           480
TrMDHi1 : CCTGATTGCTATGGTGTCTTCTGCCTTACCTATGATTGAAGGCTGAAGAGGAGACAAAAT : 485
TrMDHi2 : CCTGATTGCTATGGTGTCTTCTGCCTTACCTATGATTGAAGGCTGAAGAGGAGACAAAAT : 440

      *           500          *           520          *           540
TrMDHi1 : CCTGGAAGAAATTAATCAACATTGCAGTCTCAGGTGCTGCTGGAATGATTTCCAATCATCT : 546
TrMDHi2 : CCTGGAAGAAATTAATCAACATTGCAGTCTCAGGTGCTGCTGGAATGATTTCCAATCATCT : 501

      *           560          *           580          *           600          *
TrMDHi1 : ACTTTTCAAGCTTGCATCTGGTGAAGTTTTTGGCCCAAATCAACCTATTGCGCTGA----- : 602
TrMDHi2 : ACTTTTCAAGCTTGCATCTGGTGAAGTTTTTGGCCCAAATCAACCTATTGCGCTGAAATTA : 562

      *           620          *           640
TrMDHi1 : ----- : -
TrMDHi2 : TTAGGATCAGAAAGGTCCTTCCAAGCTCTTGAAGGTG : 599

```

Figure 82 Nucleotide sequence of TrMDHj

TrMDHj : GCAAAGCNCCTCNCNGACCTGGTGTGGAGCGAGCAGCTTTGCTAGACATAAATGGGCAGAT : 60

TrMDHj : TTTTGC GGAGCAGGGAAAAGCTCTAAATGCAGTCGCATCTCGCAATGTCAAAGTTATAGT : 120

TrMDHj : TGTGGGAAACCCCTTGCAATACAAATGCATTAATATGCTTGAAGAATGCTCCAAATATTCC : 180

TrMDHj : TGCAAAAAATTTTCATGCTTTAACCCGTTTAGATGAGAACAGAGCAAAATGTCAGCTAGC : 240

TrMDHj : CCTCAAGGCAGGTGTCTTCTACGATAAAGTGTGCAATATGACGATATGGGGAAACCACTC : 300

TrMDHj : AACTACTCAGGTCCCCGATTCTTAAATGCCAGAATCGATGGTTTGCCTGTCAAAGAAGT : 360

TrMDHj : GATTAAGGATCAAAAGTGGTTAGAGGAAGAGTTCACCGAAAAAGTTCAAAGAGAGGTGG : 420

TrMDHj : CGTGCTTATTCAAAAGTGGGGAAGATCGTCTGCTGCATCAACTTCTGTGTGCGATAGTTGA : 480

TrMDHj : TGCCATACGATCTTTGATCACTCCTACTCCGGAGGGTGATTGGTTTTCTACTGGTGTGTA : 540

TrMDHj : TACAGCTGGAAATCCTTATGGAATAGCTG : 569

Figure 83 Deduced amino acid sequence of TrMDHj

TrMDHj : * 20 * 40 * 60
 : QSXXXPGVERAALLDINGQIFABQGKALNAVASRNVKVIVVGNPCNTNALICLKNAPNIP : 60

TrMDHj : * 80 * 100 * 120
 : AKNFHALTRLDENRAKCQLALKAGVFYDKVSNMTIWGNHSTTQVPDFLNARIDGLPVKEV : 120

TrMDHj : * 140 * 160 * 180
 : IKDQKWLEEEFTEKVQKRGGVLIQKWGRSSAASTSVSIVDAIRSLITPTPEGDWFFSTGVY : 180

TrMDHj : TAGNPYGIA : 189

Figure 84 Nucleotide sequence of TrMDHk

TrMDHk : GNGTAGAACCCGTGAAGCCTTTTCCCTCCGGTCTCCCCGCTTGCGCCGTCGCCCGTCAATT : 60

TrMDHk : GCTGCTTGTGTCGTCGCCTCCAGCTCCTCCTCCTCCACTGTGCCAACC GAATTACAAACC : 120

TrMDHk : AAAAAAATGGCGACTTGTTTGCAAACACAACCTCTCCACACAAGACCTTTTCAGTTTCGG : 180

TrMDHk : TCTTCCTCGTCGACAAGACCAACTTCCCTAAGATGTTCCGCCGCCACCCCATCCACCAA : 240

TrMDHk : AAATCCTACAAAATCACTCTTCTTCCGGGTGATGGCATAGGTCTTGAAGTCGTTTCCGTC : 300

TrMDHk : GCTAAAGACGTTCTTCTCCTCACTGGATCCATCCATGGGATTAAACTTGAGTTTCAAGAG : 360

TrMDHk : AAGCTTTTGGGTGGTGCTGCTCTTGATGCTACTGGAGTTCCTTTACCTGATGATACTCTT : 420

TrMDHk : TCTGTTGCTAAGCAATCTGATGCTGTTCTTCTTGGTGCTATTGGAGGGTATAAATGGGAT : 480

TrMDHk : AAAAATGAGAAACAGCTGAAGCCAGAACTGGATTGCTTCAGCTACGAGAAGGGCTTCAA : 540

TrMDHk : GTTTTTGCTAATCTCAGA : 558

Figure 85 Deduced amino acid sequence of TrMDHk

TrMDHk : MATCLQTQLLHTRPFQFRSSSTRPTSLRCSAATPSTKKS^{*}YKITLLPGDGIGPEVVS^{*}VAK : 60

TrMDHk : DVLLLTGSIHG^{*}IKLEFQEKLLGGAALDATGVPLPDDT^{*}LSVAKQSDAVLLGAIGGYKWDKN : 120

TrMDHk : EKQLKPETG^{*}LLQLREG^{*}LQVFANLR : 144

Figure 86 Consensus contig nucleotide sequence of TrPEPCa

TrPEPCa : GNNACATTNCCGAATGCTGCTGAACTAGGGAGTGATTCCCTTGGAGCCTATGTCATCTCT : 60

TrPEPCa : ATGGCCTCAAGTGCAAGCGATGTCCTTGCAGTAGAGCTTTTACAGAAGGATGCACGTCTT : 120

TrPEPCa : ACAGTTTGTGGAGAATTAGGAAGAGCATGTCCGGGTGGAACGCTTCGGGTGGTTCCTCTA : 180

TrPEPCa : TTTGAAACTGTGCAAGACCTGAGAGGAGCTGGTGCAGTTATCAGAAAACTTTATCAATC : 240

TrPEPCa : GATTGGTACCGCCAACACATCATTAAGAACCATAACGGACACCAAGAGGTTATGGTCGGT : 300

TrPEPCa : TATTCTGATTCTGGTAAAGATGCCGGGCGCTTTACTGCTGCTTGGGAACTTTACAAAGCT : 360

TrPEPCa : CAAGAGGATGTAGTGGCTGCTTGCAATAAGTACGATACTAAGGTTACTTTGTTCCACGGC : 420

TrPEPCa : CGCGGAGGGAGTATTGGACGTGGCGGAGGCCCAACATATCTGGCTATTCAGTCCCAGCCA : 480

TrPEPCa : CCTGGCTCTGTGATGGGAACCCCTTCGGTCAACTGAGCAGGGAGAGATGGTGCAGGCCGAG : 540

TrPEPCa : TTTGGGTTGCCACAGACAGCAGTTAGACAACCTTGAAATATACACAACAGCTGTGCTACTT : 600

TrPEPCa : GCTACACGTCGTCCACCACTCCACCTCGAGAAGAAAAATGGCGTAATCTAATGGAAGAC : 660

TrPEPCa : ATNTCAAAAATCAGTTGTCAGTCCTACCGCAGTGTAGTCTATGAAAATCCAGN : 713

87 Deduced amino acid sequence of TrPEPCa

TrPEPCa : XTXPNAAELGSDSLGAYVISMASDVLAVELLQKDARLTVCGELGRACPGGTLRVVPL : 60

TrPEPCa : FETVQDLRGAGAVIRKLLSIDWYRQHIIKNHNGHQEVMVGYSKDGKAGRFTAAWELYKA : 120

TrPEPCa : QEDVVAACNKYDTKVTLFHHGRGGSIGRGGGPTYLAIQSQPPGSVMGTLRSTEQGEMVQAE : 180

TrPEPCa : FGLPQTAVRQLEIYTTAVLLATRRPPLPPREEKWRNLMEDXSKISCQSYRSVVYENP : 237

* 620

* 640

* 660

TrPEPCa1 : ----- : -
TrPEPCa2 : GCTACACGTCGTCCACCACTCCCACCTCGAGAAGAAAAATGGCGTAATCTAATGGAAGAC : 567
TrPEPCa3 : GCTACACGTCGTCCACCACTCCCACCTCGAGAAGAAAAATGGCGTAATCTAATGGAAGAC : 566

* 680

* 700

TrPEPCa1 : ----- : -
TrPEPCa2 : ATN----- : 570
TrPEPCa3 : ATTTCAAAAAATCAGTTGTCAGTCCTACCGCAGTGTAGTCTATGAAAAATCCAGN : 619

89. Consensus contig nucleotide sequence of TrPEPCb

```

      *           20           *           40           *           60
TrPEPCb : GNAAGGGACAAGCTCTATCGTACTCGTGAGCGGTCTCGCTATCTCTTAGCTCATGGCTAT : 60

      *           80           *           100          *           120
TrPEPCb : TCTGAAATTCCTGAAGAAGCCACATTACCGATGTTGATGAGTTCTTGGAACCTCTTGAA : 120

      *           140          *           160          *           180
TrPEPCb : CTATGCTACAGATCACTCTGTGCTTGTGGTGATCGTGCGATTGCCGATGGAAGCCTTCTT : 180

      *           200          *           220          *           240
TrPEPCb : GATTTCTTGAGGCAAGTTTCCACTTTTGGACTGTCACTGGTAAGACTTGATATAAGGCAA : 240

      *           260          *           280          *           300
TrPEPCb : GAGTCAGATCGTCACACGGACGTGATGGATGCCATTACCAAACATTTGGAATTTGGATCC : 300

      *           320          *           340          *           360
TrPEPCb : TACCAAGACTGGTCTGAAGAAAAAAGACAGGAATGGCTTTTGTCTGAGTTGGTTGGCAA : 360

      *           380          *           400          *           420
TrPEPCb : AGGCCGCTTTTGGACCTGACCTACCTCAAACCGATGAAATTAGAGAAGTTTATAGAGACA : 420

      *           440          *           460          *           480
TrPEPCb : TTTCATGTCATAGCAGAACTTCCATCAGACAACTTTGGAGCCTATATCATTTTCGATGGCA : 480

      *           500          *           520          *           540
TrPEPCb : ACTGCCCCGTCTGATGTGCTAGCGGTTGAACTTCTTCAACGTGAATGCAAAATCAAGAAT : 540

      *           560          *           580          *
TrPEPCb : CCGTTAAGAGTTGTTCCGTTGTTTGAGAACTTGCTGATCTCGAGTCTGCTCCTGCTG : 598

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90 Deduced amino acid sequence of TrPEPCb

TrPEPCb : XRDKLYRTRERSRYLLAHGYSEIPEEATFTDVDEFLEPLELCYRSLCACGDRAIADGSLL : 60

TrPEPCb : DFLRQVSTFGLSLVRLDIRQESDRHTDVMDAITKHLEIGSYQDWSEEKRQEWLLSELVGK : 120

TrPEPCb : RPLFGPDLPQTDEIREVLETFHVIAELPSDNFGAYIISMATAPSDVLAVELLQRECKIKN : 180

TrPEPCb : PLRVVPLFEKLADLESAPA : 199

Figure 91 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrPEPCb

	* 20 * 40 * 60	
TrPEPCb1 :	GNAAGGGACAAGCTCTATCGTACTCGTGAGCGGTCTCGCTATCTCTTAGCTCATGGCTAT	: 60
TrPEPCb2 :	CTAAGGGACAAGCTCTATCGTACTCGTGAGCGGTCTCGCTATCTCTTAGCTCATGGCTAT	: 60
	* 80 * 100 * 120	
TrPEPCb1 :	TCTGAAATTCCTGAAGAAGCCACATTCACCGATGTTGATGAGTTCTTGGAACCTCTTGAA	: 120
TrPEPCb2 :	TCTGAAATTCCTGAAGAAGCCACATTCACCGATGTTGATGAGTTCTTGGAACCTCTTGAA	: 120
	* 140 * 160 * 180	
TrPEPCb1 :	CTATGCTACAGATCACTCTGTGCTTGTGGTGATCGTGCGATTGCCGATGGAAGCCTTCTT	: 180
TrPEPCb2 :	CTATGCTACAGATCACTCTGTGCTTGTGGTGATCGTGCGATTGCCGATGGAAGCCTTCTT	: 180
	* 200 * 220 * 240	
TrPEPCb1 :	GATTTCTTGAGGCAAGTTTCCACTTTTGGACTGTCAGTGGTAAGACTTGATATAAGGCAA	: 240
TrPEPCb2 :	GATTTCTTGAGGCAAGTTTCCACTTTTGGACTGTCAGTGGTAAGACTTGATATAAGGCAA	: 240
	* 260 * 280 * 300	
TrPEPCb1 :	GAGTCAGATCGTCACACGACGTGATGGATGCCATTACCAAACATTTGGAAATTGGATCC	: 300
TrPEPCb2 :	GAGTCAGATCGTCACACGACGTGATGGATGCCATTACCAAACATTTGGAAATTGGATCC	: 300
	* 320 * 340 * 360	
TrPEPCb1 :	TACCAAGACTGGTCTGAAGAAAAAAGACAGGAATGGCTTTTGTCTGAGTTGGTTGGCAAA	: 360
TrPEPCb2 :	TACCAAGACTGGTCTGAAGAAAAAAGACAGGAATGGCTTTTGTCTGAGTTGGTTGGCAAA	: 360
	* 380 * 400 * 420	
TrPEPCb1 :	AGGCCGCTTTTGGACCTGACCTACCTCAAACCGATGAAATTAGAGAAGTTTGTAGAGACA	: 420
TrPEPCb2 :	AGGCCGCTTTTGGACCTGACCTACCTCAAACCGATGAAATTAGAGAAGTTTGTAGAGACA	: 420
	* 440 * 460 * 480	
TrPEPCb1 :	TTTCATGTCATAGCAGAACTTCCATCAGACAACCTTGGAGCCTATATCATTTTCGATGGCA	: 480
TrPEPCb2 :	TTTCATGTCATAGCAGAACTTCCATCAGACAACCTTGGAGCCTATATCATTTTCGATGGCA	: 480
	* 500 * 520 * 540	
TrPEPCb1 :	ACTGCCCCGTCTGATGTGCTAGCGGTTGAACTTCTTCAACGTGAATGCAAAATCAAGAAT	: 540
TrPEPCb2 :	ACTGCCCCGTCTGATGTGCTAGCGGTTGAACTTCTTCAACGTGAATGCAAAATCAAGAAT	: 540
	* 560 * 580 *	
TrPEPCb1 :	CCGTTAAGAGTTGTTCCGTTGTTTGAGAACTTGCTGATCTCGAGTCTGCTCCTGCTG	: 598
TrPEPCb2 :	CCGTTAAGAGTTGTTCCGTTGTTTGAGAACTTGCTGATCTCGN-----	: 584

e 92 Consensus contig nucleotide sequence of TrPEPCc

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      *           20           *           40           *           60
TrPEPCc : GTCACATGACAAACNATATCTCCCTTCTCTAACTCCGTGATCAAGGCGTTAGTTAGTTA : 60

      *           80           *           100          *           120
TrPEPCc : CACAAATTGCTGTTAGGTTTCGTTGTACTTTCCCGTGCAATCCATAGTATCTTGGAGGAA : 120

      *           140          *           160           *           180
TrPEPCc : CAAACTAGATTTTCCACCTAGGTCGTCACGAGATTTTCTCTTCACTATTTTCTTTTTC : 180

      *           200          *           220           *           240
TrPEPCc : ATATAATAACTCAACACTTTTTCTAGCTACTTACTAGTACTGTGTAACACAAATTTTATT : 240

      *           260          *           280           *           300
TrPEPCc : CATTATGGCTACTCCTCGCAACATTGAAAAAATGGCTTCAATTGATGCTCAATTGAGACT : 300

      *           320          *           340           *           360
TrPEPCc : ACTAGCACCAAGGAAAGTTTCTTGATGATGATAAACTTGTGAGTATGATGCTTTGTTATT : 360

      *           380          *           400           *           420
TrPEPCc : GGATCGATTCTTGGACATTCTTCAAGATTTGCATGGAGAAGATATCAGACAAACTGTTCA : 420

      *           440          *           460           *           480
TrPEPCc : AGATTGTTATGAGTTATCGGCAGAGTATGAAGGGGAGCTTAAGCCGGAGAAATTGGAGGA : 480

      *           500          *           520           *           540
TrPEPCc : ACTTGGGAATATGCTTACTGGTCTTGATGCTGGAGATTCTATTGTTATAGCAAATCATT : 540

      *           560          *
TrPEPCc : TTCTCATATGCTTAATTTGGCAAACCTTGGCAGAGN : 575

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93 Deduced amino acid sequence of TrPEPCc

TrPEPCc : MATPRNIEKMASIDAQLRLLAPRKVSDDDKLVEYDALLLDLDRFLDILQDLHGEDIQTVQD : 60

TrPEPCc : CYELSAEYEGELKPEKLEELGNMLTGLDAGDSIVIAKSFSHMLNLANLAE : 110

re 94 Nucleotide sequences of nucleic acid fragments contributing to the
consensus contig sequence TrPEPCc

	*	20	*	40	*	60	
TrPEPCc1 :	GTCACATGAC TT NAC TT ATATCTCCCTTTCTCTAACTCCGTGATCAAGGCGTTAGTTAGTTA						: 60
TrPEPCc2 :	-----TGACAAACNATATCTCCCTTTCTCTAACTCCGTGATCAAGGCGTTAGTTAGTTA						: 54

	*	80	*	100	*	120	
TrPEPCc1 :	CACAAATTGCTGTTAGGTTTCGTTGTACTTTCCCGTGCAATCCATAGTATCTTGGAGGAA						: 120
TrPEPCc2 :	CACAAATTGCTGTTAGGTTTCGTTGTACTTTCCCGTGCAATCCATAGTATCTTGGAGGAA						: 114

	*	140	*	160	*	180	
TrPEPCc1 :	CAAAC TAGATTTTCCACCTAGGTCGTCACGAGATTTTCCTCTTCACTATTTTTCTTTTTTC						: 180
TrPEPCc2 :	CAAAC TAGATTTTCCACCTAGGTTGTCACGAGATTTTCCTCTTCACTATTTTTCTTTTTTC						: 174

	*	200	*	220	*	240	
TrPEPCc1 :	ATATAATAACTCAACACTTTTTCTAGCTACTTACTAGTACTGTGTAAACACAAATTTTATT						: 240
TrPEPCc2 :	ATATAATAA TT TCACACTTTTTCTAGCTACTTACTAGTACTGTGTAAACACAAATTTTATT						: 234

	*	260	*	280	*	300	
TrPEPCc1 :	CATTATGGCTACTCCTCGCAACATTGAAAAAATGGCTTCAATTGATGCTCAATTGAGACT						: 300
TrPEPCc2 :	CATTATGGCTACTCCTCGCAACATTGAAAAAATGGCTTCAATTGATGCTCAATTGAGACT						: 294

	*	320	*	340	*	360	
TrPEPCc1 :	ACTAGCACCAAGGAAAGTTTCTGATGATGATAAACTTGTCGAGTATGATGCTTTGTTATT						: 360
TrPEPCc2 :	ACTAGCACCAAGGAAAGTTTCTGATGATGATAAACTTGTCGAGTATGATGCTTTGTTATT						: 354

	*	380	*	400	*	420	
TrPEPCc1 :	GGATCGATTTCCTTGACATTCTTCAAGATTGTCATGGAGAAGATATCAGACAAACTGTTCA						: 420
TrPEPCc2 :	GGATCGATTTCCTTGACATTCTTCAAGATTGTCATGGAGAAGATATCAGACAAACTGTTCA						: 414

	*	440	*	460	*	480	
TrPEPCc1 :	AGATTGTTATGAGTTATCGGCAGAGTATGAAGGGGAGCTTATGCGCGAGAAATTGGAGGA						: 480
TrPEPCc2 :	AGATTGTTATGAGTTATCGGCAGAGTATGAAGGGGAGCTTAAGCCGGAGAAATTGGAGGA						: 474

	*	500	*	520	*	540	
TrPEPCc1 :	ACTTGGGAATATGCTTACTGGTCTTGATGCTGGAGATTCTATTGTTATAGCAAAATCATT						: 540
TrPEPCc2 :	ACTTGGGAATATGCTTACTGGTCTTGATGCTGGAGATTCTATTGTTATAGCAAAATCATT						: 534

	*	560	*				
TrPEPCc1 :	TTCTCATATGCTTAATTTGGCAAACCTGGCAGAGN						: 575
TrPEPCc2 :	TTN-----						: 537

95 Nucleotide sequence of TrPEPCd

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      *           20           *           40           *           60
TrPEPCd : AGAAGATCTCATGTTTGTGTTGTCTATGTGGCGCTGCAACGACGAGCTCCGTGTTAGAGC : 60

      *           80           *           100          *           120
TrPEPCd : TGAAGAGCTTCATAGATCCTCAAAGAAAGATGCAAAACATTATATTGAGTTTGGAAACA : 120

      *           140          *           160           *           180
TrPEPCd : GATTCCTCCAAACGAGCCATATCGTGTTATTCTTGGAGGTGTGAGGGACAAACTGTATAA : 180

      *           200          *           220           *           240
TrPEPCd : TACACGTGAACGTGCTCGACAGTTATTAGCAAATGGAACCTCTGACATCCTTGAAGAGAC : 240

      *           260          *           280           *           300
TrPEPCd : AACCTTCACGAATGTTGAGCAGTTTCTGGAGCCTCTTGAACCTGTGTTATAGGTCACTTTG : 300

      *           320          *           340           *           360
TrPEPCd : TGCATGTGGTGACCGATCAATAGCAGACGGAAGCCTTCTTGATTCTTGCGACAAGTTTC : 360

      *           380          *           400           *           420
TrPEPCd : TACATTTGGACTTTCACCTGTAAGACTCGACATCCGTCAAGAGTCAGACAGGCACACAGA : 420

      *           440          *           460           *           480
TrPEPCd : CGTTATGGATGCAATTACAAAACACTTGGAGATTGGATCTTACCGAGAATGGTCGGAAGA : 480

      *           500          *           520           *           540
TrPEPCd : ACGCAGGCAGGAATGGCTCTTGTCTGAGCTTAGTGAAAAACGCCCTCTCTTCGGCCATGA : 540

      *           560          *           580           *           600
TrPEPCd : TCTTCCTAAGACAGAAGAAATTGCCGATGTTTGTAGATACCTTNCACGTNATTTCAAACT : 600

      *           620          *           640           *           660
TrPEPCd : TNCCTCANATAGCTTTGGTGCCTATATCATCTCAATGGCAACCTCCCCATCTGATGTGCT : 660

      *           680          *           700           *           720
TrPEPCd : AGCTGTCGAGCTTTTACAACGTGAATGTCATGTGAAGCAGCCGTTAANAGTTGTTCCACT : 720

      *           740          *           760           *           780
TrPEPCd : GTTTGAAAAGCTCGCCNGTCTTGAGTCTGCTCCTGCTGCGGNAGCGCGTTTTTTNTTAGA : 780

      *           800          *           820           *           840
TrPEPCd : TTGGGNCANAACCGNNNTAATGGAAAGCAGAAGTTNTGATAGGTACTCANACTNGGGAAA : 840

      *
TrPEPCd : AGATGCTGGCCGNN : 854

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e 96 Deduced amino acid sequence of TrPEPCd

TrPEPCd : EDLMFELSMWRCNDELRVRAEELHRSSKKDAKHIEFWKQIPPNEPYRVILGGVRDKLYN : 60

TrPEPCd : TRERARQLLANGTSDILEETTFTNVEQFLEPLELCYRSLCACGDRSIADGSLDFLRQVS : 120

TrPEPCd : TFGLSLVRLDIRQESDRHTDVMDAITKHLEIGSYREWSEERRQEWLLSELGKRPLFGHD : 180

TrPEPCd : LPKTEEIADVLDTXHXISXLXSXSFAYIISMATSPSDVLAVELLQRECHVKQPLXVVPL : 240

TrPEPCd : FEKLAXLESAPAAXARFXLDWXXTXKMESRSXDRYSXXGKDAGX : 283

97 Nucleotide sequence of TrPEPCe

TrPEPCe : GTTCACTGTCTCTCTGNCCAATTTTCCTCCCTTGTCTTCTTTTCTTCTTCTTCCTCGTA : 60

TrPEPCe : TCTTACTGCCTCATTACACGGGTGAGAAGGAGTGAATTGCTCCAATGGCAACAAACAAA : 120

TrPEPCe : TGGAAAAATGGCATCAATTGATGCACAGCTTAGACAATTAGTACCAGCAAAAGTTAGTG : 180

TrPEPCe : AAGATGATAAACTTATTGAGTATGATGCTTTGTTGTTGGATCGGTTTCTTGATATCCTTC : 240

TrPEPCe : AGGATTTACATGGAGAGGATCTGAAAGATTCTGTTCAAGAAGTGTATGAACTTTCTGCGG : 300

TrPEPCe : AGTATGAAAGAAAGCATGATCCTAAGAACTTGAAGAGCTCGGAAATTGATAACAAGTT : 360

TrPEPCe : TAGATGCAGGAGATTCAATTGTTGTTGCTAAGTCCTTTTCGCACATGCTTAACTTGGCCA : 420

TrPEPCe : ACTTAGCTGAAGAGGTTTCAATTGCTCATCGTGAAGGAACAAGTTGAAGAAAGGAGATT : 480

TrPEPCe : TTAGGGATGAGAGCAATGCAACTACCGAATCAGACATCGAAGAACTCTTAAGAGACTTG : 540

TrPEPCe : TGTTTAATATGAAGAAATCTCCTCAGGAAGTTNTTGATGCGTTGAAGAACCNNACCGTTG : 600

TrPEPCe : ATTTGGTTCTTACTGCTCATCCCACTCAGTCCGTTGANGNCCNCTGCTTCCCNNGCCT : 660

TrPEPCe : GGNACGGGNACCGCNCTGNCTATCNNACTGNNN : 693

98 Deduced amino acid sequence of TrPEPCe

TrPEPCe : MATNKMEEKMASIDAQLRQLVPAKVSEDDKLIEXDALLDRFLDILQDLHGEDLKDSVQEV : 60

TrPEPCe : YELSAEYERKHDPKKLEELGNLITSLDAGDSIVVAKSFSHMLNLANLAEEVQIAHRRRNK : 120

TrPEPCe : LKKGDFRDESNTTESDIEETLKRLVFNMKKSPQEVXDALKNXTVDLVLTAHPTQSVRXX : 180

TrPEPCe : LLPXAWXGXRXXYXTX : 196

99 Consensus contig nucleotide sequence of TrCSa

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      *           20           *           40           *           60
TrCSa : GNNNCNCNACCATTACATTAATNACACTTTCNCCTTTCGCCTTGTCTCTTCTCTCTCAA : 60

      *           80           *           100          *           120
TrCSa : TATAAAGACCAATTCAATTCCCAATTCTTTTGGATCCGAAATCATTCAATCTACGCGTCT : 120

      *           140          *           160           *           180
TrCSa : TCTCTCTTCTCTGCGTTTCAAACCCTAGTTGTTTTGTTGATTGATCTAAATGGCGTTCTT : 180

      *           200          *           220           *           240
TrCSa : TCGAAGCGTTTCTGCGCTTTCAAACCTACGATCTCGTGTGGGTCAACAACCTAGTCTTGC : 240

      *           260          *           280           *           300
TrCSa : TAATTCAGTTAGATGGCTCCAAACTCCAAGCTCCAGTAACACTGATCTTTATTCTGAGAT : 300

      *           320          *           340           *           360
TrCSa : GAAGGAGCTAGTTCCAGAGTATCAGGAACGTGTTAAGAAGTTGAAGAAAGACCATGGAAG : 360

      *           380          *           400           *           420
TrCSa : TGTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGGAATGAGAGGAATGACTGC : 420

      *           440          *           460           *           480
TrCSa : TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC : 480

      *           500          *           520           *           540
TrCSa : AATTCCTGACTGCCAGAAAACACTTCCAGGTGCTTTTCCTGGTGGGGAGCCTTTGCCCGA : 540

      *           560          *           580           *           600
TrCSa : GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTTCATT : 600

      *           620          *           640           *           660
TrCSa : AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC : 660

      *           680          *           700           *           720
TrCSa : ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT : 720

      *           740          *           760           *           780
TrCSa : GGAGAGTGAGTTTACAAAGGCATACGAGAGTGGGATACATAAGTCAAGGTATTGGGAGCC : 780

      *           800          *           820           *           840
TrCSa : AACTTATGAGGATAGCTTGAATTTAATTGCTCGTTTGCCTGGAATTGCTGCCTATATTTA : 840

      *           860          *           880           *           900
TrCSa : TCGACGGATATACAAGGATGGAAAAATCATACCATTGGATGATTCTTTGGATTATGGGTGC : 900

      *           920          *           940           *           960
TrCSa : AAACATGCTCACATGTTAGGATTTGATGATCCAGAAACGCTGGAGTTTATGAGGCTGTA : 960

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* -980 * 1000 * 1020
TrCSa : TATTTCTATCCATAGTGATCATGAAGGNGGCAACGTTAGTTCTCACACAGCTCACCTAGT : 1020

* 1040 * 1060 * 1080
TrCSa : TGCTAGTTCACTATCAGATCCTTATCTTGCAATTCGCAGCTGCTCTGAATGGTTTAGCTGG : 1080

* 1100 * 1120 * 1140
TrCSa : CCCACTGCATGGTTTAGCCAATCAGGAAGTTCTACGATGGATCAGAAACATAGTTAAGGA : 1140

* 1160 * 1180 * 1200
TrCSa : GTTTGGAAC TCCAAACATAAGTACAGAACAATTGAGCGACTACATTCATAAAACATTGAA : 1200

* 1220 * 1240 * 1260
TrCSa : CAGTGGCCAGGTTGTGCCTGGATATGGACATGGAGTTTTGCGCAATACAGACCCAAGATA : 1260

* 1280 * 1300
TrCSa : CACTTGCCAGAGGGAGTTTGCATTGAAGCATTGCCTAATGATCCAN : 1307

Se 100 Deduced amino acid sequence of TrCSa

TrCSa : * 20 * 40 * 60
 : MAFFRSVSALSCLRSRVGQQPSLANSVRWLQTPSSSNTDLYSEMKELVPEYQERVKKLKK : 60

TrCSa : * 80 * 100 * 120
 : DHGSVELGKITADMVLGGMRGMTALVWLGSVDPDEGIRFRGMTIPDCQKTLPGAFFPGGE : 120

TrCSa : * 140 * 160 * 180
 : PLPEAILWLLLTGKVPSEQVDSLAEHLRSRAKIPEYAYKAIDALPVSAHPMTQFSTGVM : 180

TrCSa : * 200 * 220 * 240
 : ALQVESEFTKAYESGIHKSRYWEPTYEDSLNLIARLPGIAAYIYRRIYKDGKIIPLDDSL : 240

TrCSa : * 260 * 280 * 300
 : DYGANIAHMLGFDDPETLEFMRLYISIHSDHEGNVSSHTAHLVASSLSDPYLAFAAALNG : 300

TrCSa : * 320 * 340 * 360
 : LAGPLHGLANQEVLRWIRNIVKEFGTPNISTEQLSDYIHKTLNSGQVVPGYGHGVLRNTD : 360

TrCSa : *
 : PRYTCQREFALKHLPNDP : 378

Figure 101 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrCSa

		*	20	*	40	*	60		
TrCSa1 :	GNNNCN	CNACCATTAC	GTTAATTACA	TTTCTT	CTTTTCGCCTT	GTTCTTT	TCTCTTCTCAA	:	60
TrCSa2 :	-----	ACATTG	CTNA	TCTT	CTTTTCGCCTT	GTTCTTT	TCTCTTCT-AA	:	45
TrCSa3 :	-----	-----	-----	-----	-----	-----	-----	:	-
TrCSa4 :	-----	-----	-----	-----	-----	-----	-----	:	-
TrCSa5 :	-----	-----	-----	-----	-----	-----	-----	:	-
TrCSa6 :	-----	-----	-----	-----	-----	-----	-----	:	-
TrCSa7 :	-----	-----	-----	-----	-----	-----	-----	:	-
		*	80	*	100	*	120		
TrCSa1 :	TATAAAGACCAATTCAATTCCCAATTCTTTTGGATCCGAAATCATTCA	TTCTACGCTTCT	:	120					
TrCSa2 :	TATAAAGACC-ATTCAATTCCCAATTCTTTTGGATCCGAAATCATTCA	TTCTACGCTTCT	:	104					
TrCSa3 :	-----TACCGNAAC-TTTCTTNC-TACTTTTNCACGCTTNC	CT	:	40					
TrCSa4 :	-----	-----	:	10					
TrCSa5 :	-----	-----	:	-					
TrCSa6 :	-----	-----	:	-					
TrCSa7 :	-----	-----	:	-					
		*	140	*	160	*	180		
TrCSa1 :	TCTCTCTTCTCTGCGTTTCAAACCCTAGTTGTTTTGTTGATTGATCT	TAATGGCGTTCTT	:	180					
TrCSa2 :	TCTCTCTTCTCTGCGTTTCAAACCCTAGTTGTTTTGTTGATTGATCT	TAATGGCGTTCTT	:	164					
TrCSa3 :	TCTCTCTTCTCTGCGTTTCAAACCCTAGTTGTTTTGTTGATTGATCT	TAATGGCGTTCTT	:	100					
TrCSa4 :	TCTCTCTTCTCTGCGTTTCAAACCCTAGTTGTTTTGTTGATTGATCT	TAATGGCGTTCTT	:	67					
TrCSa5 :	-----	-----	:	-					
TrCSa6 :	-----	-----	:	-					
TrCSa7 :	-----	-----	:	-					
		*	200	*	220	*	240		
TrCSa1 :	TCGAAGCGTTTCTGCGCTTTCAAACCTACGATCTCGTGTGGGTCAACA	ACCTAGTCTTGC	:	240					
TrCSa2 :	TCGAAGCGTTTCTGCGCTTTCAAACCTACGATCTCGTGTGGGTCAACA	ACCTAGTCTTGC	:	224					
TrCSa3 :	TCGAAGCGTTTCTGCGCTTTCAAACCTACGATCTCGTGTGGGTCAACA	ACCTAGTCTTGC	:	160					
TrCSa4 :	TCGAAGCGTTTCTGCGCTTTCAAACCTACGATCTCGTGTGGGTCAACA	ACCTAGTCTTGC	:	127					
TrCSa5 :	-----	-----	:	-					
TrCSa6 :	-----	-----	:	-					
TrCSa7 :	-----	-----	:	-					
		*	260	*	280	*	300		
TrCSa1 :	TAATTCAGTTAGATGGCTCCAAACTCCAAGCTCCAGTAACACTGATCTT	TATTCTGAGAT	:	300					
TrCSa2 :	TAATTCAGTTAGATGGCTCCAAACTCCAAGCTCCAGTAACACTGATCTT	TATTCTGAGAT	:	284					
TrCSa3 :	TAATTCAGTTAGATGGCTCCAAACTCCAAGCTCCAGTAACACTGATCTT	TATTCTGAGAT	:	220					
TrCSa4 :	TAATTCAGTTAGATGGCTCCAAACTCCAAGCTCCAGTAACACTGATCTT	TATTCTGAGAT	:	187					
TrCSa5 :	-----	-----	:	-					
TrCSa6 :	-----	-----	:	-					
TrCSa7 :	-----	-----	:	-					
		*	320	*	340	*	360		
TrCSa1 :	GAAGGAGCTAGTTCCAGAGTATCAGGAACGTGTTAAGAAGTTGAAGAA	GACCATGGAAG	:	360					
TrCSa2 :	GAAGGAGCTAGTTCCAGAGTATCAGGAACGTGTTAAGAAGTTGAAGAA	GACCATGGAAG	:	344					
TrCSa3 :	GAAGGAGCTAGTTCCAGAGTATCAGGAACGTGTTAAGAAGTTGAAGAA	GACCATGGAAG	:	280					
TrCSa4 :	GAAGGAGCTAGTTCCAGAGTATCAGGAACGTGTTAAGAAGTTGAAGAA	GACCATGGAAG	:	247					
TrCSa5 :	-----	-----	:	-					
TrCSa6 :	-----	-----	:	-					
TrCSa7 :	-----	-----	:	-					

	*	380	*	400	*	420	
TrCSa1 :		TGTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGAATGAGAGGAATGACTGC				:	420
TrCSa2 :		TGTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGAATGAGAGGAATGACTGC				:	404
TrCSa3 :		TGTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGAATGAGAGGAATGACTGC				:	340
TrCSa4 :		TGTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGAATGAGAGGAATGACTGC				:	307
TrCSa5 :		-----GNGGAAAAATCACAGCTGATATGGTACTTGGTGAATGAGAGGAATGACTGC				:	51
TrCSa6 :		-----GNGGAAAAATCACAGCTGATATGGTACTTGGTGAATGAGAGGAATGACTGC				:	16
TrCSa7 :		-----				:	-

	*	440	*	460	*	480	
TrCSa1 :		TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC				:	480
TrCSa2 :		TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC				:	464
TrCSa3 :		TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC				:	400
TrCSa4 :		TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC				:	367
TrCSa5 :		TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC				:	111
TrCSa6 :		TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC				:	74
TrCSa7 :		-----				:	-

	*	500	*	520	*	540	
TrCSa1 :		AATTCCTGACTGCCAGAAAACACTTCCAGGTGCTTTTCTGGTGGGGAGCCTTTGCCCGA				:	540
TrCSa2 :		AATTCCTGACTGCCAGAAAACACTTCCAGGTGCTTTTCTGGTGGGGAGCCTTTGCCCGA				:	524
TrCSa3 :		AATTCCTGACTGCCAGAAAACACTTCCAGGTGCTTTTCTGGTGGGGAGCCTTTGCCCGA				:	460
TrCSa4 :		AATTCCTGACTGCCAGAAAACACTTCCAGGTGCTTTTCTGGTGGGGAGCCTTTGCCCGA				:	427
TrCSa5 :		AATTCCTGACTGCCAGAAAACACTTCCAGGTGCTTTTCTGGTGGGGAGCCTTTGCCCGA				:	171
TrCSa6 :		AATTCCTGACTGCCAGAAAACACTTCCAGGTGCTTTTCTGGTGGGGAGCCTTTGCCCGA				:	133
TrCSa7 :		-----				:	-

	*	560	*	580	*	600	
TrCSa1 :		GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTTCATT				:	600
TrCSa2 :		GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTTCATT				:	584
TrCSa3 :		GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTTCATT				:	520
TrCSa4 :		GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTTCATT				:	456
TrCSa5 :		GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTTCATT				:	231
TrCSa6 :		GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTTCATT				:	193
TrCSa7 :		-----				:	-

	*	620	*	640	*	660	
TrCSa1 :		AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC				:	660
TrCSa2 :		AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC				:	588
TrCSa3 :		AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC				:	580
TrCSa4 :		-----				:	-
TrCSa5 :		AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC				:	291
TrCSa6 :		AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC				:	253
TrCSa7 :		-----				:	-

	*	680	*	700	*	720	
TrCSa1 :		ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGCCCCTCCAGGT				:	692
TrCSa2 :		-----				:	-
TrCSa3 :		ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGCCCCTCCAGGT				:	640
TrCSa4 :		-----				:	-
TrCSa5 :		ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGCCCCTCCAGGT				:	351
TrCSa6 :		ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGCCCCTCCAGGT				:	313
TrCSa7 :		-----				:	-

	*	740	*	760	*	780	
TrCSa1 :	-----						-
TrCSa2 :	-----						-
TrCSa3 :	-----						681
TrCSa4 :	-----						-
TrCSa5 :	-----						411
TrCSa6 :	-----						373
TrCSa7 :	-----						34

	*	800	*	820	*	840	
TrCSa1 :	-----						-
TrCSa2 :	-----						-
TrCSa3 :	-----						-
TrCSa4 :	-----						-
TrCSa5 :	-----						471
TrCSa6 :	-----						433
TrCSa7 :	-----						92

	*	860	*	880	*	900	
TrCSa1 :	-----						-
TrCSa2 :	-----						-
TrCSa3 :	-----						-
TrCSa4 :	-----						-
TrCSa5 :	-----						531
TrCSa6 :	-----						493
TrCSa7 :	-----						152

	*	920	*	940	*	960	
TrCSa1 :	-----						-
TrCSa2 :	-----						-
TrCSa3 :	-----						-
TrCSa4 :	-----						-
TrCSa5 :	-----						591
TrCSa6 :	-----						553
TrCSa7 :	-----						212

	*	980	*	1000	*	1020	
TrCSa1 :	-----						-
TrCSa2 :	-----						-
TrCSa3 :	-----						-
TrCSa4 :	-----						-
TrCSa5 :	-----						601
TrCSa6 :	-----						581
TrCSa7 :	-----						272

	*	1040	*	1060	*	1080	
TrCSa1 :	-----						-
TrCSa2 :	-----						-
TrCSa3 :	-----						-
TrCSa4 :	-----						-
TrCSa5 :	-----						-
TrCSa6 :	-----						-
TrCSa7 :	-----						332

* 1100 * 1120 * 1140

TrCSa1 : ----- : -
TrCSa2 : ----- : -
TrCSa3 : ----- : -
TrCSa4 : ----- : -
TrCSa5 : ----- : -
TrCSa6 : ----- : -
TrCSa7 : CCCACTGCATGGTTTAGCCAATCAGGAAGTTCTACGATGGATCAGAAAATAGTTAAGGA : 392

* 1160 * 1180 * 1200

TrCSa1 : ----- : -
TrCSa2 : ----- : -
TrCSa3 : ----- : -
TrCSa4 : ----- : -
TrCSa5 : ----- : -
TrCSa6 : ----- : -
TrCSa7 : GTTTGGAACCTCCAAACATAAGTACAGAACAATTGAGCGACTACATTCATAAAACATTGAA : 452

* 1220 * 1240 * 1260

TrCSa1 : ----- : -
TrCSa2 : ----- : -
TrCSa3 : ----- : -
TrCSa4 : ----- : -
TrCSa5 : ----- : -
TrCSa6 : ----- : -
TrCSa7 : CAGTGGCCAGGTTGTGCCTGGATATGGACATGGAGTTTTGCGCAATACAGACCCAAGATA : 512

* 1280 * 1300

TrCSa1 : ----- : -
TrCSa2 : ----- : -
TrCSa3 : ----- : -
TrCSa4 : ----- : -
TrCSa5 : ----- : -
TrCSa6 : ----- : -
TrCSa7 : CACTTGCCAGAGGGAGTTTGCATTGAAGCATTTGCCTAATGATCCAN : 559

102 Consensus contig nucleotide sequence of TrCSb

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      *           20           *           40           *           60
TrCSb : C N T T T C N T T T C C A C A G C A T C C T A A T C C T A A T C C T A A T C C T A T T A C T A A T T A C T A : 60

      *           80           *           100          *           120
TrCSb : A T T A C T A A T T A C T A G T A C T A A T T A G T A A T A C C G A T C C C T T T T T C T G A A C C C A T T C A T T C : 120

      *           140          *           160          *           180
TrCSb : A A G N A G A A G A A G G A A A A C A A A A T C C A C A C A A A C A A C A T C T T A C A A C A A T G T C A A C G A C : 180

      *           200          *           220          *           240
TrCSb : A A C T A C T A C A A C C G A C G A A T C C A A G C T G C A C G A C G C T G C A C G G A A C C G T T T G G C C A C C C T : 240

      *           260          *           280          *           300
TrCSb : C T C A G C T C A C T T G C T T C C T T C C T C C A C A C C T C C G C C G C T C C T C C A T C C T A T T C A C C T : 300

      *           320          *           340          *           360
TrCSb : T T C T T C T T C C T C C G G A T C T C C C C A C C G T C T A A T G T C A A A G G A A C A C T C A C C G T T G T T G A : 360

      *           380          *           400          *           420
TrCSb : T G A A C G T A C C G G G A A G A A G T A T A C C A T T G A G G T C T C T C C T G A T G G C A C C G T T A A A G C C A A : 420

      *           440          *           460          *           480
TrCSb : T G A T T T C A A G A A G A T A T C A A C T G G G A A G A A T G A T A A G G G A C T C A A A C T T T A T G A T C C T G G : 480

      *           500          *           520          *           540
TrCSb : A T A T T T A A A C A C T G C T C C T G T G C G A T C A A C A A T T T C T T A T A T T G A T G G T G A T G A G G G A A T : 540

      *           560          *           580          *           600
TrCSb : C C T T A G A T A T A G A G G A T A C C C C A T T G A G G A G T T G G C C G A G A A A A G C A C C T T T C C G G A A G T : 600

      *           620          *           640          *           660
TrCSb : G G C A T A T C T C A T A T T G T A T G G A A A T T T G C C T T C T G C A A A T C A G T T A C A A G A A T G G G A A T T : 660

      *           680          *           700          *           720
TrCSb : T G C T A T A T C T C A G C A T T C A G C C T T A C C T C A A G G A G T T T T G G A T C T C A T A C A A T C A A T G C C : 720

      *           740          *           760          *           780
TrCSb : T C A A G A T G C A C A T C C T A T G G G C G T C C T A G T G A A T G C A A T A A G C G C T C T G T C T G T T T T T C A : 780

      *           800          *           820          *           840
TrCSb : T C C T G A C G C A A A T C C T G C T C T C A G A G G T C T T G A C A T C T A C A A C T C A A A G C A A G T G A G A G A : 840

      *           860          *           880          *           900
TrCSb : C A A A C A A A T A G C A C G G A T T A T T G G A A G A T A A C A C A A T T G C T G C T G C A A T T A A T C T T A G : 900

      *           920          *           940          *           960
TrCSb : A A T G G C A G G A A G G C C A C C T G T G C T T C C A T C C A A C A A A C T A T C T T A C A C A G A G A A C T T C C T : 960

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* 980 * 1000 * 1020
TrCSb : ATACATGCTTGATTCTCTAGGCAATCGGTTCATATAAACCCAACCCTCAGCTAACTCGTGC : 1020

* 1040 * 1060 * 1080
TrCSb : ACTAGACATCATCTTCATCCTGCATGCAGAACATGAAATGAATTGCTCTACATCTGCTGT : 1080

* 1100 * 1120 * 1140
TrCSb : ACGACACCTTGTCATCAAGCGGCGTCGATGTATACACTGCTATTGCTGGAGGTGTTGGAGC : 1140

* 1160 * 1180 * 1200
TrCSb : TCTGTATGGACCTCTTCATGGTGGAGCTAATGAGGCGGTCCTTAAAATGCTGAGTGAAAT : 1200

* 1220 * 1240
TrCSb : TGGAAGTGTCGATAACATTCCAGAGTTCATTGAAGGTGTTAANN : 1244

103 Deduced amino acid sequence of TrCSb

TrCSb : M S T T T T T T D E S K L H D A A R N R L A T L S A H L L P S S T T S A A L L H P I H L S S S S G I S P P S N V K G T L : 60

TrCSb : T V V D E R T G K K Y T I E V S P D G T V K A N D F K K I S T G K N D K G L K L Y D P G Y L N T A P V R S T I S Y I D G : 120

TrCSb : D E G I L R Y R G Y P I E E L A E K S T F P E V A Y L I L Y G N L P S A N Q L Q E W E F A I S Q H S A L P Q G V L D L I : 180

TrCSb : Q S M P Q D A H P M G V L V N A I S A L S V F H P D A N P A L R G L D I Y N S K Q V R D K Q I A R I I G K I T T I A A A : 240

TrCSb : I N L R M A G R P P V L P S N K L S Y T E N F L Y M L D S L G N R S Y K P N P Q L T R A L D I I F I L H A E H E M N C S : 300

TrCSb : T S A V R H L A S S G V D V Y T A I A G G V G A L Y G P L H G G A N E A V L K M L S E I G S V D N I P E F I E G V X : 358

Figure 104 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrCSb

	*	20	*	40	*	60	
TrCSb1 :	CNTTTCNTTTCACAGCATCCTAATCCTAATCCTAATCCTAATCCTATTACTAATTACTA	:	60				
TrCSb2 :	-----	:	-				
TrCSb3 :	-----	:	-				
TrCSb4 :	-----	:	-				
TrCSb5 :	-----	:	-				
TrCSb6 :	-----	:	-				
TrCSb7 :	-----	:	-				
	*	80	*	100	*	120	
TrCSb1 :	ATTACTAATTACTAGTACTAATTAGTAATACCGATCCCTTTTCTCGAACCATTTCATTC	:	120				
TrCSb2 :	-----	:	-				
TrCSb3 :	-----	:	-				
TrCSb4 :	-----	:	-				
TrCSb5 :	-----	:	-				
TrCSb6 :	-----	:	-				
TrCSb7 :	-----	:	-				
	*	140	*	160	*	180	
TrCSb1 :	AAATTCNAAGAAGGAAAAACAAAT-CACACAAACAAACATCTTACAACAATGTCAACGAC	:	179				
TrCSb2 :	--GNAGNAGAAGGAAACNC-AAAATCCACAAC-AAAAC-TCTTACAACAATGTCAACGAC	:	55				
TrCSb3 :	--GNNGNAGAAGGAAACACAAAATNCACAAACAAACATCTTACAACAATGTCAACGAC	:	58				
TrCSb4 :	---GNAAAGAGGAAAAAC-AAAT--NCACAAAC-AACATCTTAC-ACAATGTC-ACGAC	:	50				
TrCSb5 :	---GNAAGGAAAAAC-AAAT--NC-CAAC-AAC-TCTTAC-ACAATGTC-ACGAC	:	45				
TrCSb6 :	-----	:	-				
TrCSb7 :	-----	:	-				
	*	200	*	220	*	240	
TrCSb1 :	AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTGGCTACCCT	:	239				
TrCSb2 :	AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTGGCCACCCT	:	115				
TrCSb3 :	AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTGGCCACCCT	:	118				
TrCSb4 :	AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTGGCCACCCT	:	110				
TrCSb5 :	AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTGGCTACCCT	:	105				
TrCSb6 :	-----	:	-				
TrCSb7 :	-----	:	-				
	*	260	*	280	*	300	
TrCSb1 :	CTCAGCTCACTTGCTTCCTTCCTCCACAACTCCGCTGGCGCTCTCCATCCTATCACCT	:	299				
TrCSb2 :	CTCAGCTCACTTGCTTCCTTCCTCCACAACCTCCGCGCGCTCCTCCATCCTATTACCT	:	175				
TrCSb3 :	CTCAGCTCACTTGCTTCCTTCCTCCACAACCTCCGCGCGCTCCTCCATCCTATTACCT	:	178				
TrCSb4 :	CTCAGCTCACTTGCTTCCTTCCTCCACAACCTCCGCGCGCTCCTCCATCCTATTACCT	:	170				
TrCSb5 :	CTCAGCTCACTTGCTTCCTTCCTCCACAACTCCGCTGGCGCTCTCCATCCTATCACCT	:	165				
TrCSb6 :	-----	:	-				
TrCSb7 :	-----	:	-				
	*	320	*	340	*	360	
TrCSb1 :	TTCTTCTTCCTCTGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTGACCGTTGTTGA	:	359				
TrCSb2 :	TTCTTCTTCCTCTCGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTGACCGTTGTTGA	:	235				
TrCSb3 :	TTCTTCTTCCTCTCGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTGACCGTTGTTGA	:	238				
TrCSb4 :	TTCTTCTTCCTCTCGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTGACCGTTGTTGA	:	230				
TrCSb5 :	TTCTTCTTCCTCTGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTGACCGTTGTTGA	:	225				
TrCSb6 :	-----	:	-				
TrCSb7 :	-----	:	-				

	*	380	*	400	*	420	
TrCSb1 :		TGAACGTACCGGGAAGAAGTATAACCATTTGAGGTCTCTCCTGATGGCACCGTTAAAGCCAA					: 419
TrCSb2 :		TGAACGTACCGGGAAGAAGTATAACCATTTGAGGTCTCTCCTGATGGCACCGTTAAAGCCAA					: 295
TrCSb3 :		TGAACGTACCGGGAAGAAGTATAACCATTTGAGGTCTCTCCTGATGGCACCGTTAAAGCCAA					: 298
TrCSb4 :		TGAACGTACCGGGAAGAAGTATAACCATTTGAGGTCTCTCCTGATGGCACCGTTAAAGCCAA					: 290
TrCSb5 :		TGAACGTACCGGGAAGAAGTATAACCATTTGAGGTCTCTCCTGATGGCACCGTTAAAGCCAA					: 285
TrCSb6 :		-----					: -
TrCSb7 :		-----					: -

	*	440	*	460	*	480	
TrCSb1 :		TGATTTCAAGAAGATATCAACTGGGAAGAATGATAAGGGCTCAAACCTTTATGATCCTGG					: 479
TrCSb2 :		TGATTTCAAGAAGATATCAACTGGGAAGAATGATAAGGGCTCAAACCTTTATGATCCTGG					: 355
TrCSb3 :		TGATTTCAAGAAGATATCAACTGGGAAGAATGATAAGGGCTCAAACCTTTATGATCCTGG					: 358
TrCSb4 :		TGATTTCAAGAAGATATCAACTGGGAAGAATGATAAGGGCTCAAACCTTTATGATCCTGG					: 350
TrCSb5 :		TGATTTCAAGAAGATATCAACTGGGAAGAATGATAAGGGCTCAAACCTTTATGATCCTGG					: 345
TrCSb6 :		-----					: -
TrCSb7 :		-----					: 1

	*	500	*	520	*	540	
TrCSb1 :		ATATTTAAACACTGCTCCTGTGCGATCAACAATTTCTTATATTGATGGTGATGAGGGAAT					: 539
TrCSb2 :		ATATTTAAACACTGCTCCTGTGCGATCAACAATTTCTTATATTGATGGTGATGAGGGAAT					: 415
TrCSb3 :		ATATTTAAACACTGCTCCTGTGCGATCAACAATTTCTTATATTGATGGTGATGAGGGAAT					: 418
TrCSb4 :		ATATTTAAACACTGCTCCTGTGCGATCAACAATTTCTTATATTGATGGTGATGAGGGAAT					: 410
TrCSb5 :		ATATTTAAACACTGCTCCTGTGCGATCAACAATTTCTTATATTGATGGTGATGAGGGAAT					: 405
TrCSb6 :		-----					: -
TrCSb7 :		-----					: -

	*	560	*	580	*	600	
TrCSb1 :		CCTTAGATATAGAGGATACCCATTGAGAGTTGGCCGAGAAAAGCACCTTTCCGGAAGT					: 599
TrCSb2 :		CCTTAGATATAGAGGATACCCATTGAGAGTTGGCCGAGAAAAGCACCTTTCCGGAAGT					: 475
TrCSb3 :		CCTTAGATATAGAGGATACCCATTGAGAGTTGGCCGAGAAAAGCACCTTTCCGGAAGT					: 478
TrCSb4 :		CCTTAGATATAGAGGATACCCATTGAGAGTTGGCCGAGAAAAGCACCTTTCCGGAAGT					: 470
TrCSb5 :		CCTTAGATATAGAGGATACCCATTGAGAGTTGGCCGAGAAAAGCACCTTTCCGGAAGT					: 465
TrCSb6 :		-----ATAGAGGCT-----CCNATTGAGGAGTTGG-----CGAGAAAAGCACCTTTATGGAAGT					: 49
TrCSb7 :		-----					: -

	*	620	*	640	*	660	
TrCSb1 :		GGCATATCT-----					: 609
TrCSb2 :		GGCATATCTCATATTGTATGGAAATTTGCCTTCTGCAAATCAGTTACAAGAATGGGAATT					: 535
TrCSb3 :		GGCATATCTCATATTGTATGGAAATTTGCCTTCTGCAAATCAGTTACAAGAATGGGAATT					: 538
TrCSb4 :		GGCATATCTCATATTGTATGGAAATTTGCCTTCTGCAAATCAGTTACAAGAATGGGAATT					: 530
TrCSb5 :		GGCATATCTCATATTGTATGGAAATTTGCCTTCTGCAAATCAGTTACAAGAATGGGAATT					: 525
TrCSb6 :		GGCATATCT-----ATAATGTATGGAAATTTACCTACTGAAAGTAAGTTAGCTGAATGGAAATT					: 108
TrCSb7 :		-----					: 12

	*	680	*	700	*	720	
TrCSb1 :		-----					: -
TrCSb2 :		TGCTATATCTCAGCATTACGCTTACCTCAAGGAGTTTTGGATCTCATACAATN-----					: 589
TrCSb3 :		TGCTATATCTCAGCATTACGCTTACCTCAAGGAGTTTTGGATCTCATACAATC-----					: 594
TrCSb4 :		TGCTATATCTCAGCATTACGCTTACCTCAAGGAGTTTTGGATCTCATACAATCAATGCC					: 570
TrCSb5 :		TGCTATATCTCAGCATTACGCTTACCTCAAGGAGTTTTGGATCTCATACAATCAATGCC					: 585
TrCSb6 :		GGCTATATCTCAGCATTACGCTTACCTCAAGGAGTTTTGGATCTCATACAATCAATGCC					: 168
TrCSb7 :		TGCTATATCT-AGCATT-AGCCTTACCTCAAGGAGTTTTGGATCTCATACAATCAATGCC					: 70

	*	740	*	760	*	780	
TrCSb1 :	-----		-----		-----		-
TrCSb2 :	-----		-----		-----		-
TrCSb3 :	-----		-----		-----		-
TrCSb4 :	-----		-----		-----		-
TrCSb5 :	TCAAGNN		-----		-----		592
TrCSb6 :	TCAAGATGCACATCCTATGGGCTCTAGTGAATGCAATAAGCGCTCTTCTGTTTTTCA		-----		-----		228
TrCSb7 :	TCAAGATGCACATCCTATGGGCGTCTTGTGAATGCTCTAAGTCTTGTCTGTTTTTCA		-----		-----		130

	*	800	*	820	*	840	
TrCSb1 :	-----		-----		-----		-
TrCSb2 :	-----		-----		-----		-
TrCSb3 :	-----		-----		-----		-
TrCSb4 :	-----		-----		-----		-
TrCSb5 :	-----		-----		-----		-
TrCSb6 :	TCCTGACGC	AAATCCTGCTCT		AGAGGTCTTGATAT		TACGACTCAAAGCAAGTGAGAGA	288
TrCSb7 :	TCCTGAGCA	AAATCCTGCTCT		CAGAGGTCTTGACATCTACA		ACTCAAAGCAAGTGAGAGA	190

	*	860	*	880	*	900	
TrCSb1 :	-----		-----		-----		-
TrCSb2 :	-----		-----		-----		-
TrCSb3 :	-----		-----		-----		-
TrCSb4 :	-----		-----		-----		-
TrCSb5 :	-----		-----		-----		-
TrCSb6 :	CAAACAAATAGCACGGATTATTGGAAAGAT		AAACAATTGCTGCTGCACTT		TATCTTAG		348
TrCSb7 :	CAAACAAATAG		CGGATTATTGGAAAGATAACA		CAATTGCTGCTGCC		250

	*	920	*	940	*	960	
TrCSb1 :	-----		-----		-----		-
TrCSb2 :	-----		-----		-----		-
TrCSb3 :	-----		-----		-----		-
TrCSb4 :	-----		-----		-----		-
TrCSb5 :	-----		-----		-----		-
TrCSb6 :	AATGGCAGGAAGGCCACCTGTGCTTCCATCCAAC		CAACTATCTTACAC		GGAGAACTTCCT		408
TrCSb7 :	AATGGCAGGAAGGCCACCTGT		CTTCCATCCAACAACT		TCTTACACAGAGAACTTCCT		310

	*	980	*	1000	*	1020	
TrCSb1 :	-----		-----		-----		-
TrCSb2 :	-----		-----		-----		-
TrCSb3 :	-----		-----		-----		-
TrCSb4 :	-----		-----		-----		-
TrCSb5 :	-----		-----		-----		-
TrCSb6 :	ATACATGCTTGATTCT		TAGGCAATCGGT		CATATAAACCCAACTTCAGCTAACTCGTGC		468
TrCSb7 :	ATACATGCTTGATTCTCT		TGGCAATCGGT		CATATAAACCTAACTTCAGCTAACTCGTGC		370

	*	1040	*	1060	*	1080	
TrCSb1 :	-----		-----		-----		-
TrCSb2 :	-----		-----		-----		-
TrCSb3 :	-----		-----		-----		-
TrCSb4 :	-----		-----		-----		-
TrCSb5 :	-----		-----		-----		-
TrCSb6 :	ACTAGACAT		TATCTTCATCCTGCATGCAGAACATGAAATGAATTGCTCTACATCTGCTGT				528
TrCSb7 :	ACTAGACATCATCTTCATCCT		TCATGCAGAACATGAAATGAATTGCTCTACATCTGCTGT				430

	*	1100	*	1120	*	1140	
TrCSb1 :		-----		-----		-----	: -
TrCSb2 :		-----		-----		-----	: -
TrCSb3 :		-----		-----		-----	: -
TrCSb4 :		-----		-----		-----	: -
TrCSb5 :		-----		-----		-----	: -
TrCSb6 :		CCGACACCTTGCATCAAGCGGCGTGGATGTATATACTGCTATTGCTGGGCGN					: 579
TrCSb7 :		ACGACACCTTGCATCAAGTGGTGTCTGATGTATACACTGCTATTGCTGGAGGTGTTGGAGC					: 490

	*	1160	*	1180	*	1200	
TrCSb1 :		-----		-----		-----	: -
TrCSb2 :		-----		-----		-----	: -
TrCSb3 :		-----		-----		-----	: -
TrCSb4 :		-----		-----		-----	: -
TrCSb5 :		-----		-----		-----	: -
TrCSb6 :		-----		-----		-----	: -
TrCSb7 :		TCTGTATGGACCTCTTCATGGTGGAGCTAATGAGGCGGTCCTTAAAATGCTGAGTGAAAT					: 550

	*	1220	*	1240	
TrCSb1 :		-----		-----	: -
TrCSb2 :		-----		-----	: -
TrCSb3 :		-----		-----	: -
TrCSb4 :		-----		-----	: -
TrCSb5 :		-----		-----	: -
TrCSb6 :		-----		-----	: -
TrCSb7 :		TGGAAGTGTCTGATAACATTCCAGAGTTCATTGAAGGTGTTAANN			: 594